

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 32.5277 Seconds
(without alignments)
1284.140 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSSLSASVGRVT.....HQVSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	100.0	108	4	AAB81986
2	571	99.5	128	4	AAB81996
3	570	99.3	128	4	AAB81993
4	564	98.3	128	4	AAB81997
5	561	97.7	128	4	AAB81995
6	558	97.2	128	4	AAB81994
7	557	97.0	128	4	AAB81992
8	557	97.0	108	6	ABU11011 Modified
9	548	95.5	108	4	AAB81988
10	548	95.5	128	4	AAB81999
11	548	95.5	128	4	AAB81998
12	533	92.9	110	2	AAW70673 Anti-VEGF
13	533	92.9	110	5	ABP61242 Humanised
14	533	92.9	237	2	AAW70703 Protein e
15	533	92.9	650	5	ABP61241 Phage-dis
16	531	92.5	107	2	AAW86805 Variable
17	531	92.5	107	2	AAW70625 Humanised
18	531	92.5	107	5	ABP61194 Humanised
19	530	92.3	110	2	AAW70675 Anti-VEGF
20	530	92.3	110	5	ABP61244 Humanised
21	529	92.2	108	2	AAW70618 Anti-VEGF
22	529	92.2	108	5	ABP61187 Humanised
23	529	92.2	108	8	ADG31782 V(L) doma
24	529	92.2	108	8	ADG31768 V(L) doma
25	529	92.2	108	8	ADG31893 V(L) prot

26	529	92.2	110	3	AAB05897
27	529	92.2	110	3	AAB13376 F(ab)-12
28	529	92.2	237	8	ADQ90721 Anti-VEGF
29	527	91.8	107	2	AAW86804 Variable
30	527	91.8	107	2	AAW70623 Humanised
31	527	91.8	107	5	ABP61192 Humanised
32	526	91.6	108	8	ADG31770 V(L) doma
33	526	91.6	110	2	AAW70677 Anti-VEGF
34	526	91.6	110	2	AAW70687 Anti-VEGF
35	526	91.6	110	3	AAB13380 Anti-VEGF
36	526	91.6	110	5	ABP61256 Humanised
37	526	91.6	110	5	ABP61246 Humanised
38	526	91.6	214	7	ADC26154 Parent an
39	526	91.6	237	5	ABP51952 Plasmid p
40	526	91.6	237	5	ABP51952 Plasmid p
41	526	91.6	237	8	ADQ14128 Plasmid p
42	526	91.6	237	8	ADQ14131 Plasmid p
43	526	91.6	237	8	ADQ90703 Anti-VEGF
44	526	91.6	237	8	ADQ90701 Anti-VEGF
45	526	91.6	237	8	ADQ90705 Anti-VEGF
46	526	91.6	237	8	ADQ90709 Anti-VEGF
47	526	91.6	237	8	ADQ90723 Anti-VEGF
48	526	91.6	237	8	ADQ90707 Anti-VEGF
49	523	91.1	108	5	ABP70696 Humanised
50	523	91.1	108	5	ABP61265 Humanised
51	510	88.9	108	3	AAW56678 Anti-inte
52	510	88.9	246	8	ADH50845 SGI11 var
53	509	88.7	214	7	ADC26157 Anti-VEGF
54	508	88.5	214	7	ADC26156 Anti-VEGF
55	507	88.3	108	8	ADN41877 Humanised
56	507	88.3	110	2	AAW70685 Anti-VEGF
57	507	88.3	110	2	AAW70681 Anti-VEGF
58	507	88.3	110	2	AAW70683 Anti-VEGF
59	507	88.3	110	2	AAW70679 Anti-VEGF
60	507	88.3	110	3	AAW05898 Humanised
61	507	88.3	110	3	AAW13386 Anti-VEGF
62	507	88.3	110	3	AAW13387 Anti-VEGF
63	507	88.3	110	3	AAW13388 Anti-VEGF
64	507	88.3	110	5	ABP61250 Humanised
65	507	88.3	110	5	ABP61252 Humanised
66	507	88.3	110	5	ABP61254 Humanised
67	506	88.2	127	2	AAW11817 Humanised
68	506	88.2	127	2	AAW60035 Human ant
69	506	88.2	214	2	AAW34504 Light cha
70	506	88.2	214	2	AAW34506 Light cha
71	506	88.2	214	2	AAW95615 Humanized
72	506	88.2	214	2	AAW30632 Recombina
73	506	88.2	214	2	AAW08754 Human ant
74	506	88.2	214	4	AAW66777 rhuMab CD
75	506	88.2	214	5	ABG31889 Humanised
76	506	88.2	214	8	ADK18342 Amino aci
77	506	88.2	233	2	AAW30777 pH52-9.0
78	506	88.2	237	2	AAW95622 pS1130 ex
79	506	88.2	237	2	AAW30634 Recombina
80	506	88.2	237	2	AAW66784 Protein e
81	506	88.2	237	6	ABP72745 Anti-CD18
82	506	88.2	246	8	ADH50847 SGV RFB4
83	506	88.2	246	8	ADH50846 SGIV RFB4
84	506	88.2	246	8	ADH50846 SGIV RFB4
85	504	87.8	110	5	ABP61248 Humanised
86	503	87.6	103	7	ADP09995 Antibody
87	503	87.6	103	7	ADP10099 VEGF anti
88	503	87.6	214	2	AAW43338 Completel
89	503	87.6	214	2	AAW49815 Amino aci
90	503	87.6	214	6	AAW49815 Amino aci
91	503	87.6	214	6	ADN49727 Human imm
92	502	87.5	246	8	ADH50844 SGI11 RFB
93	501	87.3	108	2	AAW70622 Human con
94	501	87.3	108	3	AAW82345 Human con
95	501	87.3	108	5	ABP61191 Human ant
96	501	87.3	108	8	ADG38991 Human con
97	501	87.3	108	8	ADG3366 Human sub
98	501	87.3	108	8	ADP79572 Human kap

99	501	87.3	109	5	AAU74544	Aau74544 Human sub
100	501	87.3	110	5	AAE28149	Aae28149 Human con

ALIGNMENTS

XX	RESULT 1
XX	AAB81986
XX	ID AAB81986 standard; protein; 108 AA.
XX	AC AC
XX	AAB81986;
XX	03-JUL-2001 (first entry)
XX	Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX	Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX	cancer.
XX	OS Synthetic.
XX	WO200123432-A1.
XX	05-APR-2001.
XX	29-SEP-2000; 2000WO-JP006774.
XX	30-SEP-1999; 99JP-00278291.
XX	06-APR-2000; 2000JP-00105088.
XX	(KYOW) KYOWA HAKKO KOGYO KK.
XX	Hanai N, Shitara K, Nakamura K, Niwa R;
XX	WPI; 2001-266143/27.
XX	New human type complementation-determining region-transplanted antibody
XX	PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX	PT of e.g. tumors, with low antigenicity, little side effects but potent
XX	PT activity in cancer.
XX	Example 1; Page 143-144; 183pp; Japanese.
XX	The present invention describes a monoclonal antibody which can react
XX	CC specifically with ganglioside GD3. The antibody and its derivatives are
XX	CC useful in the diagnosis and therapy of tumours, particularly cancer
XX	CC diagnosis. The present sequence is a protein used in the exemplification
XX	CC of the invention
XX	SQ Sequence 108 AA;

RESULT 2
AAB81996
ID AAB81996 standard; protein; 128 AA.
XX
AC AAB81996;
XX
DT 03-JUL-2001 (first entry)

DE	Ganglioside GD3 specific antibody related protein #5.
XX	
KW	Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW	cancer.
XX	
OS	Synthetic.
XX	
XX	WO200123432-A1.
XX	
XX	05-APR-2001.
XX	
XX	29-SEP-2000; 2000WO-JP006774.
XX	
XX	30-SEP-1999; 99JP-00278291.
PR	06-APR-2000; 2000JP-00105088.
XX	
XX	(KYOW) KYOWA HAKKO KOGYO KK.
PA	
XX	
PI	Hanai N, Shitara K, Nakamura K, Niwa R;
XX	
XX	WPI; 2001-266143/27.
DR	N-PSDB; AAP86904.
DR	
XX	
PT	New human type complementation-determining region-transplanted antibody
PT	and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT	of e.g. tumors, with low antigenicity, little side effects but potent
PT	activity in cancer.
XX	
PS	Example 1; Page 159-160; 183pp; Japanese.
XX	
CC	The present invention describes a monoclonal antibody which can react
CC	specifically with ganglioside GD3. The antibody and its derivatives are
CC	useful in the diagnosis and therapy of tumors, particularly cancer
CC	diagnosis. The present sequence is a protein used in the exemplification
CC	of the invention
XX	
SQ	Sequence 128 AA;
	Query Match 99.5%; Score 571; DB 4; Length 128;
	Best Local Similarity 99.1%; Pred. No. 2.5e-34;
	Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps
Qy	1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFYSNLHSGVPS 60
Db	21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFYSNLHSGVPS 80
Qy	61 RFSGGGSGTDYLTITSSLOPEFATYYCHQYSKLPWTFGQGTKEIKR 108
Db	81 RFSGGGSGTDYLTITSNLQPEFATYYCHQYSKLPWTFGQGTKEIKR 128
RESULT 3	
AAB81993	
ID	AAB81993 standard; protein; 128 AA.
XX	
AC	AAB81993;
XX	
XX	
DT	03-JUL-2001 (first entry)
XX	
XX	Ganglioside GD3 specific antibody related protein #2.
DE	
XX	Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW	cancer.
KW	
XX	
OS	Synthetic.
OS	
XX	
XX	WO200123432-A1.
XX	
XX	05-APR-2001.
PD	
XX	
XX	29-SEP-2000; 2000WO-JP006774.
PF	
XX	
XX	30-SEP-1999; 99JP-00278291.
PR	

RESULT 3	
AA81993	
ID	AA81993 standard; protein; 128 AA.
XX	
XX	
AC	AA81993;
XX	
DT	03-JUL-2001 (first entry)
XX	
DE	Ganglioside GD3 specific antibody related protein #2.
XX	
KW	Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW	Cancer.
XX	
XX	Synthetic.
OS	
XX	
PN	WO200123432-A1.
XX	
XX	
PD	05-APR-2001.
XX	
XX	
PF	29-SEP-2000; 2000WO-JF006774.
XX	
XX	
PR	30-SEP-1999; 99JP-00278291.

PS Example 1; Page 161-162; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX
SQ Sequence 128 AA;

Query Match 98.3%; Score 564; DB 4; Length 128;
Best Local Similarity 98.1%; Pred. No. 8.2e-34;
Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPKGKAPKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPKGKAPKLLIFYSSNLHSGVPS 60
Qy 61 RFSGGSGTDYTLTITSSLOPEFATYCHQYSKLPWTFGQGTQKVIKR 108
Db 81 RFSGGSGTDYTLTITSSLOPEFATYCHQYSKLPWTFGQGTQKVIKR 128

RESULT 5

AAB81995
ID AAB81995 standard; protein; 128 AA.
XX
AC AAB81995;
XX
DT 03-JUL-2001 (first entry)
XX
DE DE
XX
KW Ganglioside GD3 specific antibody related protein #4.
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI: 2001-266143/27.
DR N-PSDB; AAF86901.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 1; Page 157-158; 183pp; Japanese.

PS
SQ The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX
SQ Sequence 128 AA;

Query Match 97.7%; Score 561; DB 4; Length 128;
Best Local Similarity 97.2%; Pred. No. 1.3e-33;
Matches 105; Conservative 2; Mismatches 1; Indels 0; Gaps

```
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db |||||
QY 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80
Db |||||

QY 61 RFSGGSGGTDYTLTITSSLPEDFATYYCHQYSKLPWTFCQGTKEIKR 108
Db |||||

RESULT 6
AAB81994
ID AAB81994 standard; protein; 128 AA.
XX
AC AAB81994;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #3.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
DR N-PSDB; AAF86898.
XX
New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 155-156; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 97.2%; Score 558; DB 4; Length 128;
Best Local Similarity 98.1%; Pred. No. 2.2e-33;
Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db |||||
QY 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80
Db |||||

QY 61 RFSGGSGGTDYTLTITSSLPEDFATYYCHQYSKLPWTFCQGTKEIKR 108
Db |||||

RESULT 7
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
AC AAB81992;
XX
```

```
XX 03-JUL-2001 (first entry)
DT
XX Ganglioside GD3 specific antibody related protein #1.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KW
XX Synthetic.
OS
XX WO200123432-A1.
PN
XX 05-APR-2001.
PD
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
DR N-PSDB; AAF86892.
XX
New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 150-151; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 97.2%; Score 558; DB 4; Length 128;
Best Local Similarity 97.2%; Pred. No. 2.2e-33;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db |||||
QY 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80
Db |||||

QY 61 RFSGGSGGTDYTLTITSSLPEDFATYYCHQYSKLPWTFCQGTKEIKR 108
Db |||||

QY 81 RFSGGSGGTDYTLTITSSLPEDFATYYCHQYSKLPWTFCQGTKEIKR 128
Db |||||

RESULT 8
AAB11011
ID AAB11011 standard; protein; 108 AA.
XX
AC AAB11011;
XX
DT 04-FEB-2003 (first entry)
XX
DE Modified ganglioside GD3 antibody associated protein #4.
XX
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS Synthetic.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-JP003170.
XX
```


XX 29-MAR-2001; 2001JP-00097483.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Claim 8; Page 100; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumor
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 108 AA;
XX
XX Query Match 97.0%; Score 557; DB 6; Length 108;
XX Best Local Similarity 97.2%; Pred. No. 2.3e-33;
XX Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 DIQMTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60
XX 1 DIQMTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60
XX 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108
XX 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108
XX
XX RESULT 9
XX AAB81988
XX ID AAB81988 standard; protein; 108 AA.
XX AC AAB81988;
XX XX
XX 03-JUL-2001 (first entry)
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX Synthetic.
XX WO200123432-A1.
XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-JP006774.
XX 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.

XX Claim 22; Page 172-173; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumours, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX Sequence 108 AA;
XX
XX Query Match 95.5%; Score 548; DB 4; Length 108;
XX Best Local Similarity 96.3%; Pred. No. 1e-32;
XX Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 DIQMTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60
XX 1 DIQMTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60
XX 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108
XX 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108
XX
XX RESULT 10
XX AAB81999
XX ID AAB81999 standard; protein; 128 AA.
XX AC AAB81999;
XX XX
XX 03-JUL-2001 (first entry)
XX Ganglioside GD3 specific antibody related protein #8.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX Synthetic.
XX WO200123432-A1.
XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-JP006774.
XX 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX N-PSDB; AAF86913.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX
XX Example 1; Page 166; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumours, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX Sequence 128 AA;
XX
XX Query Match 95.5%; Score 548; DB 4; Length 128;
XX Best Local Similarity 96.3%; Pred. No. 1.2e-32;
XX Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 80
QY 61 RFSGGSGGTDYTLTITSSLPQEDFATYCHQYKSLPWTFCGGTKVEIKR 108
DB 81 RFSGGSGGTDYTLTITSSLPQEDFATYCHQYKSLPWTFCGGTKVEIKR 128

RESULT 11
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
AC AAB81998;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #7.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX
New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 3; Page 164-165; 183pp; Japanese.
XX
The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 95.5%; Score 548; DB 4; Length 128;
Best Local Similarity 96.3%; Pred. No. 1.2e-32;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 80
QY 61 RFSGGSGGTDYTLTITSSLPQEDFATYCHQYKSLPWTFCGGTKVEIKR 108
DB 81 RFSGGSGGTDYTLTITSSLPQEDFATYCHQYKSLPWTFCGGTKVEIKR 128

RESULT 12
AAW70673
ID AAW70673 standard; peptide; 110 AA.
XX
```

```
AC AAW70673;
XX
DT 27-JAN-1999 (first entry)
XX
DE Anti-VEGF humanised antibody variable light domain of template MB1.6.
XX
KW Light variable domain; murine; humanised antibody;
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW VEGF-induced angiogenesis; tumour; retinal disorder;
KW age-related macular degeneration; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO9845331-A2.
XX
PD 15-OCT-1998.
XX
PF 03-APR-1998; 98WO-US006604.
XX
PR 07-APR-1997; 97US-00833504.
PR 06-AUG-1997; 97US-00908469.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
WPI; 1998-568337/48.
XX
New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
Example 3; Fig 9A; 100pp; English.
XX
The present sequence represents a variable light domain of the template
CC molecule of the affinity-matured anti-vascular endothelial growth factor
CC (anti-VEGF) antibody. The sequence is used in the course of the invention
CC to produce the humanised anti-VEGF antibody of the invention. The
CC humanised antibodies are used to inhibit VEGF-induced angiogenesis,
CC particularly for treating or preventing tumours (of any type) and retinal
CC disorders (e.g. age-related macular degeneration or diabetic
CC retinopathy). They can also be used to treat other conditions that
CC involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX
SQ Sequence 110 AA;
Query Match 92.9%; Score 533; DB 2; Length 110;
Best Local Similarity 91.7%; Pred. No. 1.3e-31;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFSGGSGGTDYTLTITSSLPQEDFATYCHQYKSLPWTFCGGTKVEIKR 108
DB 61 RFSGGSGGTDYTLTITSSLPQEDFATYCHQYKSLPWTFCGGTKVEIKR 108

RESULT 13
ABP61242
ID ABP61242 standard; protein; 110 AA.
XX
AC ABP61242;
XX
DT 20-SEP-2002 (first entry)
XX
DE Humanised anti-VEGF MB1.6 antibody variable light domain.
XX
```

KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intraocular neovascular disorder; MB1.6; light chain;
 KW variable domain.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX Key Location/Qualifiers
 XX Domain 24..34
 FT /label= CDR-L1
 FT Domain 50..57
 FT /label= CDR-L2
 FT Domain 89..97
 FT /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.
 XX (WELL/) WELLS J A.
 XX (PRES/) PRESTA L G.
 XX (LOWM/) LOWMAN H B.
 XX (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 2002-517920/55.

XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 FT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 FT mammal, particularly for treating tumor or retinal disorders.

XX Example 3; Fig 9; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human).
 CC particularly those having a tumour or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention

XX Sequence 110 AA;

Query Match 92.9%; Score 533; DB 5; Length 110;
 Best Local Similarity 91.7%; Pred. No. 1.3e-31;
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60
 Db 1 DIQLTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60

QY 61 RFSGGSGTDYTLTITSSLPEDPATYVCHQYKLPWTFGGQTKVEIKR 108
 Db 61 RFSGGSGTDYTLTITSSLPEDPATYVCHQYKLPWTFGGQTKVEIKR 108

RESULT 14

AAW70703
 ID AAW70703 standard; protein; 237 AA.

XX AAW70703;

XX 27-JAN-1999 (first entry)

XX Protein encoded by Fab-display antibody vector pHMB4-19-1.6.

XX Murine; humanised antibody; VEGF-induced angiogenesis; tumour;
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KW retinal disorder; age-related macular degeneration; diabetic retinopathy;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

OS Synthetic.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX N-PSDB; AAV63493.

XX New humanised antibody with affinity for vascular endothelial growth
 FT factor - for treatment of tumours, retinal disease and other angiogenic
 FT states, also related nucleic acid, vectors and transformed cells.

XX Example 3; Fig 8A-E; 100pp; English.

XX The present sequence is encoded by the Fab-display antibody vector pHMB4-
 CC 19-1.6, which is used in the course of the invention. The specification
 CC describes humanised murine anti-vascular endothelial growth factor (anti-
 CC VEGF) antibodies. The humanised antibodies are used to inhibit VEGF-
 CC induced angiogenesis, particularly for treating or preventing tumours (of
 CC any type) and retinal disorders (e.g. age-related macular degeneration
 CC or diabetic retinopathy). They can also be used to treat other conditions
 CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
 CC atherosclerosis, Grave's disease, etc

XX Sequence 237 AA;

Query Match 92.9%; Score 533; DB 2; Length 237;
 Best Local Similarity 91.7%; Pred. No. 2.6e-31;
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60
 Db 24 DIQLTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 83

QY 61 RFSGGSGTDYTLTITSSLPEDPATYVCHQYKLPWTFGGQTKVEIKR 108

Db 84 RFSGGSGTDYTLTITSSLPEDPATYVCHQYKLPWTFGGQTKVEIKR 131

RESULT 15

ABP61241

XX ID ABP61241 standard; protein; 650 AA.

XX AC ABP61241;

XX 20-SEP-2002 (first entry)

XX Phage-display antibody vector pHMB4-19-1.6 protein.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intraocular neovascular disorder; pHMB4-19-1.6.

XX Synthetic.

XX Key Location/Qualifiers
 FT Peptide 1..23

```
FT Protein /label= Signal_peptide
FT 24..237
FT /label= Light_chain_region
FT Peptide 238..260
FT /label= Signal_peptide
FT Protein 261..491
FT /label= Heavy_chain_region
FT /note= "Fused to g3p domain"
FT Misc-difference 492
FT /note= "Encoded by stop codon"
FT 493
FT Protein /label= Truncated g3p_domain.protein
FT /note= "Fused to heavy_chain"
FT
XX
PN US2002032315-A1.
XX
XX 14-MAR-2002.
XX
XX 06-APR-1998; 98US-00056160.
XX
XX 06-AUG-1997; 97US-0054856P.
XX
XX (BACA/) BACA M.
XX (WELL/) WELLS J A.
XX (PRES/) PRESTA L G.
XX (LOWN/) LOWMAN H B.
XX (CHEN/) CHEN Y M.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX WPI: 2002-517920/55.
XX N-PSDB; ABN85200.
XX
XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
XX mammal, particularly for treating tumor or retinal disorders.
XX
XX Example 3; Fig 8; 47pp; English.
XX
XX The present invention relates to humanised anti-VEGF (vascular
XX endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX particularly those having a tumour or a retinal disorder e.g. intraocular
XX neovascular disorders. The present sequence is the protein encoded by
XX phage-display antibody vector pMB4-19-1.6. This sequence was used as a
XX parent during the construction of humanised antibody pY101. In the pMB4
XX -19-1.6 construct, anti-VEGF is expressed as a Fab fragment with its
XX heavy chain fused to the N-terminus of the truncated g3p. Both the light
XX and heavy chains are under the control of phoA promoter with an upstream
XX still signal-sequence for secretion into the periplasm
XX
SQ Sequence 650 AA;
Query Match 92.9%; Score 533; DB 5; Length 650;
Best Local Similarity 91.7%; Pred. No. 6.4e-31; Indels 0; Gaps 0;
Matches 99; Conservative 6; Mismatches 3;
QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLHGVP 83
QY 61 RFSGGSGGTDYTLTITSSLPEDPATYCHQYKLPWTFCGGTKVEIKR 108
DB 84 RFSGGSGGTDYTLTITSSLPEDPATYCHQYKLPWTFCGGTKVEIKR 131
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Search completed: August 1, 2005, 09:10:03
Job time : 35.5277 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 8.1913 Seconds
(without alignments)
983.287 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSLASVGRVT.....HOYSLKLPWTFGGTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfilesi.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533	92.9	491	4	US-10-011-125A-2
2	529	92.2	110	4	US-09-440-781-94
3	507	88.3	110	4	US-09-440-781-95
4	506	88.2	107	2	US-07-934-373C-17
5	506	88.2	107	3	US-08-437-642B-17
6	506	88.2	107	4	US-08-146-206C-17
7	506	88.2	107	4	US-09-705-686-17
8	506	88.2	107	4	US-09-705-392A-17
9	506	88.2	107	5	PCT-US93-07832-17
10	506	88.2	109	2	US-07-934-373C-47
11	506	88.2	109	3	US-08-437-642B-47
12	506	88.2	109	3	US-08-437-642B-47
13	506	88.2	127	3	US-08-649-100-33
14	506	88.2	214	2	US-07-934-373C-40
15	506	88.2	214	2	US-08-788-800-11
16	506	88.2	214	3	US-08-437-642B-40
17	506	88.2	214	3	US-09-097-309-2
18	506	88.2	214	3	US-09-097-171A-2
19	506	88.2	214	3	US-09-460-587-2
20	506	88.2	214	4	US-09-940-166A-2
21	506	88.2	214	5	PCT-US93-07832-40
22	506	88.2	233	2	US-07-934-373C-25
23	506	88.2	233	3	US-08-437-642B-25
24	506	88.2	233	4	US-08-146-206C-25
25	506	88.2	233	4	US-09-705-686-25
26	506	88.2	233	4	US-09-705-392A-25
27	506	88.2	233	4	US-09-705-398-25

28	506	88.2	233	5	PCT-US93-07832-25	Sequence 25, Appl
29	506	88.2	237	3	US-09-097-309-6	Sequence 6, Appl
30	506	88.2	237	3	US-09-097-171A-10	Sequence 10, Appl
31	506	88.2	237	3	US-09-422-712B-2	Sequence 2, Appl
32	506	88.2	237	3	US-09-607-756-2	Sequence 2, Appl
33	506	88.2	237	3	US-09-460-587-6	Sequence 6, Appl
34	506	88.2	237	4	US-09-940-166A-6	Sequence 6, Appl
35	503	87.6	214	1	US-08-458-516-12	Sequence 12, Appl
36	501	87.3	108	3	US-08-974-899-3	Sequence 3, Appl
37	501	87.3	108	4	US-09-795-798-3	Sequence 3, Appl
38	498	86.8	107	1	US-08-458-516-8	Sequence 8, Appl
39	498	86.8	214	2	US-07-934-373C-39	Sequence 39, Appl
40	498	86.8	214	3	US-08-437-642B-39	Sequence 39, Appl
41	498	86.8	214	5	PCT-US93-07832-39	Sequence 39, Appl
42	496	86.4	107	2	US-07-934-373C-18	Sequence 18, Appl
43	496	86.4	107	2	US-08-652-558-2	Sequence 2, Appl
44	496	86.4	107	3	US-08-437-642B-18	Sequence 18, Appl
45	496	86.4	107	4	US-08-146-206C-18	Sequence 18, Appl
46	496	86.4	107	4	US-09-648-067A-14	Sequence 14, Appl
47	496	86.4	107	4	US-09-705-686-18	Sequence 18, Appl
48	496	86.4	107	4	US-09-705-392A-18	Sequence 18, Appl
49	496	86.4	107	4	US-09-705-398-18	Sequence 18, Appl
50	496	86.4	107	5	PCT-US93-07832-18	Sequence 18, Appl
51	494	86.1	128	4	US-09-225-322B-10	Sequence 10, Appl
52	494	86.1	128	4	US-09-225-322B-19	Sequence 19, Appl
53	494	86.1	128	4	US-09-764-304-10	Sequence 10, Appl
54	494	86.1	128	4	US-09-764-304-19	Sequence 19, Appl
55	492	85.7	107	3	US-09-254-189-1	Sequence 1, Appl
56	492	85.7	109	2	US-07-934-373C-3	Sequence 3, Appl
57	492	85.7	109	3	US-08-437-642B-3	Sequence 3, Appl
58	492	85.7	109	4	US-08-146-206C-3	Sequence 3, Appl
59	492	85.7	109	4	US-09-705-686-3	Sequence 3, Appl
60	492	85.7	109	4	US-09-705-392A-3	Sequence 3, Appl
61	492	85.7	109	4	US-09-705-398-3	Sequence 3, Appl
62	492	85.7	109	5	PCT-US93-07832-3	Sequence 3, Appl
63	491	85.5	105	3	US-09-199-149-31	Sequence 31, Appl
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66	491	85.5	126	1	US-08-137-117D-71	Sequence 71, Appl
67	491	85.5	126	2	US-08-436-717-71	Sequence 71, Appl
68	491	85.5	212	4	US-10-011-125A-5	Sequence 5, Appl
69	489	85.2	109	4	US-09-802-083-4	Sequence 4, Appl
70	488	85.0	109	3	US-09-157-370-3	Sequence 3, Appl
71	486.5	84.8	114	5	PCT-US95-01219-43	Sequence 43, Appl
72	486.5	84.8	114	5	US-08-561-521-43	Sequence 43, Appl
73	482	84.0	102	3	US-09-199-149-10	Sequence 10, Appl
74	482	84.0	108	3	US-09-199-149-14	Sequence 14, Appl
75	481	83.8	108	3	US-09-025-769B-14	Sequence 14, Appl
76	481	83.8	108	4	US-09-490-070A-14	Sequence 14, Appl
77	481	83.8	108	4	US-09-490-153-14	Sequence 14, Appl
78	481	83.8	108	4	US-09-490-324-14	Sequence 14, Appl
79	478	83.3	107	2	US-08-318-157B-6	Sequence 6, Appl
80	478	83.3	107	4	US-09-253-794-6	Sequence 6, Appl
81	478	83.3	127	3	US-08-836-561-71	Sequence 71, Appl
82	478	83.3	127	4	US-09-434-122-71	Sequence 71, Appl
83	477	83.1	234	4	US-09-740-002-24	Sequence 24, Appl
84	474	82.6	111	2	US-08-887-352B-7	Sequence 7, Appl
85	474	82.6	111	3	US-09-109-207C-7	Sequence 7, Appl
86	474	82.6	111	3	US-09-296-005-7	Sequence 7, Appl
87	474	82.6	111	4	US-09-920-171-7	Sequence 7, Appl
88	474	82.6	111	4	US-09-716-028-7	Sequence 7, Appl
89	474	82.6	111	4	US-10-113-996-7	Sequence 7, Appl
90	474	82.6	127	4	US-09-809-739-10	Sequence 10, Appl
91	474	82.6	218	5	PCT-US96-13152-2	Sequence 2, Appl
92	474	82.6	263	3	US-09-069-821-3	Sequence 3, Appl
93	474	82.6	263	4	US-09-956-086-3	Sequence 3, Appl
94	474	82.6	263	4	US-09-956-087-3	Sequence 3, Appl
95	474	82.6	283	3	US-09-420-592A-6	Sequence 6, Appl
96	474	82.6	283	4	US-09-985-442-6	Sequence 6, Appl
97	474	82.6	283	4	US-09-983-580-6	Sequence 6, Appl
98	472.5	82.3	114	1	US-08-202-047-25	Sequence 25, Appl
99	472.5	82.3	114	3	US-08-964-690-25	Sequence 25, Appl
100	472.5	82.3	116	1	US-08-478-039-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1

US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

Query Match 92.9%; Score 533; DB 4; Length 491;
Best Local Similarity 91.7%; Pred. No. 4.8e-43;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 24 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 83
QY 61 RFGSGSGTDYTLTISSLPEDPATYCHQYSKLPWTFGQGTKEIKR 108
DB 84 RFGSGSGTDYTLTISSLPEDPATYCHQYSKLPWTFGQGTKEIKR 131

RESULT 2

US-09-440-781-94
; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match 92.2%; Score 529; DB 4; Length 110;
Best Local Similarity 90.7%; Pred. No. 2.2e-43;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFGSGSGTDYTLTISSLPEDPATYCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFGSGSGTDYTLTISSLPEDPATYCHQYSKLPWTFGQGTKEIKR 108

RESULT 3

US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match 88.3%; Score 507; DB 4; Length 110;
Best Local Similarity 85.2%; Pred. No. 2.7e-41;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCRANEQLSNLYNMYQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFGSGSGTDYTLTISSLPEDPATYCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFGSGSGTDYTLTISSLPEDPATYCHQYSKLPWTFGQGTKEIKR 108

RESULT 4

US-07-934-373C-17
; Sequence 17, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881

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; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-17

Query Match      88.2%; Score 506; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDINSYLNWYQKPGKAPKLLIFYSNNLHSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
   |||||

QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||

RESULT 5
US-08-437-642B-17
; Sequence 17, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-17

Query Match      88.2%; Score 506; DB 3; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDINSYLNWYQKPGKAPKLLIFYSNNLHSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
   |||||

QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||

RESULT 6
US-08-146-206C-17
; Sequence 17, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-17

Query Match      88.2%; Score 506; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDINSYLNWYQKPGKAPKLLIFYSNNLHSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
   |||||

QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||

RESULT 7
US-09-705-686-17
; Sequence 17, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
```

;; TITLE OF INVENTION: Method for Making Humanized Antibodies
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/705,686
;; FILING DATE: 02-No. 6639055-2000
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146206
;; FILING DATE: 17-NOV-1993
;; APPLICATION NUMBER: 07/715272
;; FILING DATE: 14-JUN-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709PID3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;;
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-705-686-17
;
Query Match 88.2%; Score 506; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNHLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDIRNLYNWYQKPGKAPKLLIYTSRLSGVPS 60
;
QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFGQGTKEIK 107
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQGNLTPWTFGQGTKEIK 107
;
RESULT 8
US-09-705-392A-17
; Sequence 17, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-No. 6719971
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;

;; APPLICATION NUMBER: US/09/705,392A
;; FILING DATE: 02-No. 6719971-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146206
;; FILING DATE: 17-NOV-1993
;; APPLICATION NUMBER: 07/715272
;; FILING DATE: 14-JUN-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709PID1 REVISED
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;;
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-705-392A-17
;
Query Match 88.2%; Score 506; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNHLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDIRNLYNWYQKPGKAPKLLIYTSRLSGVPS 60
;
QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFGQGTKEIK 107
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQGNLTPWTFGQGTKEIK 107
;
RESULT 9
US-09-705-398-17
; Sequence 17, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-No. 6800738-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-705-398-17

Query Match 88.2%; Score 506; DB 4; Length 107;
 Best Local Similarity 89.7%; Pred. No. 3.3e-41;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINYNLWYQKPGKAPKLLIFVSSNLHSGVPS 60
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYVTSRLESGVPS 60
 Qy 61 RFGSGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGGQTKVEIK 107
 Db 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGNLPLPWTFFGGQTKVEIK 107

RESULT 10
 PCT-US93-07832-17
 ; Sequence 17, Application PC/TUS9307832
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/07832
 ; FILING DATE: 19930820
 ; CLASSIFICATION:
 ; PRIOR APPLICATION NUMBER: 07/715272
 ; FILING DATE: 14-JUN-1991
 ; APPLICATION NUMBER: PCT/US92/05126
 ; FILING DATE: 15-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/934373
 ; FILING DATE: 21-AUG-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME:
 ; REGISTRATION NUMBER:
 ; REFERENCE/DOCKET NUMBER: 709P2PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE:
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; PCT-US93-07832-17

Query Match 88.2%; Score 506; DB 5; Length 107;
 Best Local Similarity 89.7%; Pred. No. 3.3e-41;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINYNLWYQKPGKAPKLLIFVSSNLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYVTSRLESGVPS 60
 Qy 61 RFGSGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGGQTKVEIK 107
 Db 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGNLPLPWTFFGGQTKVEIK 107

RESULT 11
 US-07-934-373C-47
 ; Sequence 47, Application US/07934373C
 ; Patent No. 5821337
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul J. Carter
 ; APPLICANT: Leonard G. Presta
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/934,373C
 ; FILING DATE: 21-Aug-1992
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/05126
 ; FILING DATE: 15-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/715272
 ; FILING DATE: 14-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0709P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 47:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 109 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-07-934-373C-47

Query Match 88.2%; Score 506; DB 2; Length 109;
 Best Local Similarity 89.8%; Pred. No. 3.4e-41;
 Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINYNLWYQKPGKAPKLLIFVSSNLHSGVPS 60
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYVTSRLESGVPS 60
 Qy 61 RFGSGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGGQTKVEIK 108
 Db 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGNLPLPWTFFGGQTKVEIK 108

RESULT 12
 US-08-437-642B-47
 ; Sequence 47, Application US/08437642B
 ; Patent No. 6054297
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul J. Carter
 ; APPLICANT: Leonard G. Presta

```
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-437-642B-47
;
; Query Match 88.2%; Score 506; DB 3; Length 109;
; Best Local Similarity 89.8%; Pred. No. 3.4e-41;
; Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
;
; QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIYFSSNLSHGVP 60
; DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDISNNYLNWYQKPGKAPKLLIYTTLSHGVP 60
;
; QY 61 RFSGGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108
; DB 61 RFSGGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGQGTKEIKR 108
;
; RESULT 13
; US-08-649-100-33
; Sequence 33, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO. MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; METHOD OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
;
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-649-100-33
;
; Query Match 88.2%; Score 506; DB 3; Length 127;
; Best Local Similarity 87.9%; Pred. No. 4e-41;
; Matches 94; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
;
; QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIYFSSNLSHGVP 60
; DB 21 DIQMTQSPSTLSASVGDRTVITCRASQDISNYLNWYQKPGKAPKLLIYTTLSHGVP 80
;
; QY 61 RFSGGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIK 107
; DB 81 RFSGGSGTNYTLTISSLPDDFATYFCQGSSTLPWTFGQGTKEVK 127
;
; RESULT 14
; US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
```

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-40

Query Match 88.2%; Score 506; DB 2; Length 214;
Best Local Similarity 89.8%; Pred. No. 7.2e-41;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Qy 61 RFSGSGSGTDYTLTISSSLQPEDFATYYCHQYSKLPWTFGGGTKEIKR 108
Db 61 RFSGSGSGTDYTLTISSSLQPEDFATYYCQGGNTLPTPTFGGTKEIKR 108

RESULT 15

US-08-788-800-11
Sequence 11, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-11

Query Match 88.2%; Score 506; DB 2; Length 214;
Best Local Similarity 89.8%; Pred. No. 7.2e-41;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Qy 61 RFSGSGSGTDYTLTISSSLQPEDFATYYCHQYSKLPWTFGGGTKEIKR 108
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Search completed: August 1, 2005, 09:20:50
Job time : 10.1991 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 28.4953 Seconds
(without alignments)
1476.651 Million cell updates/sec

Title: US-10-089-500-10
Perfect score: 574
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*

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22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

US-09-056-160B-103

; Sequence 103, Application US/09056160B

; Patent No. US20020032315A1

; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel

; APPLICANT: Wells, James A.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Lowman, Henry B.

; APPLICANT: Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

; NUMBER OF SEQUENCES: 131

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/056,160B

; FILING DATE: 06-Apr-1998

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/054,856

; FILING DATE: 06-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: P1093R2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1896

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 103:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 110 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-09-056-160B-103

Query Match

Best Local Similarity 92.9%; Score 533; DB 9; Length 110;

Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60

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QY 61 RPSGGSGTDTLTITSSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

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US-10-234-671-101

; Sequence 101, Application US/10234671

; Publication No. US20030190317A1

; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel

; APPLICANT: Wells, James A.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Lowman, Henry B.

; APPLICANT: Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

; NUMBER OF SEQUENCES: 131

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/234,671

; FILING DATE: 03-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/056160

; FILING DATE: 06-APR-1998

; APPLICATION NUMBER: 60/126446

; FILING DATE: 07-APR-1997

; APPLICATION NUMBER: 60/054856

; FILING DATE: 06-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Cui, Steven X.

; REGISTRATION NUMBER: 44,637

; REFERENCE/DOCKET NUMBER: P1093R2C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

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; SEQUENCE CHARACTERISTICS:

; LENGTH: 110 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

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US-10-234-671-101

Query Match

Best Local Similarity 92.9%; Score 533; DB 14; Length 110;

Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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US-10-974-591-101

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;               Lowman, Henry B.
;               Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-974-591-101
;
; Query Match          92.9%; Score 533; DB 17; Length 110;
; Best Local Similarity 91.7%; Pred. No. 5.3e-37;
; Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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; QY 1 DIQMTSPSSLASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60
;    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; Db 1 DIQLTQSPSSLASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYTSSLHSGVPS 60
;
; QY 61 RFSGGSGTDYTLTITSSLPEDPATYVCHYQSKLPWTFGGKTVEIKR 108
;    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; Db 61 RFSGGSGTDYTLTITSSLPEDPATYVCHYQSKLPWTFGGKTVEIKR 108
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; RESULT 4
US-09-056-160B-100
; Sequence 100, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
;
; Query Match          92.9%; Score 533; DB 9; Length 237;
; Best Local Similarity 91.7%; Pred. No. 1.1e-36;
; Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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; QY 1 DIQMTSPSSLASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60
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; Db 24 DIQLTQSPSSLASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYTSSLHSGVPS 83
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; QY 61 RFSGGSGTDYTLTITSSLPEDPATYVCHYQSKLPWTFGGKTVEIKR 108
;    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; Db 84 RFSGGSGTDYTLTITSSLPEDPATYVCHYQSKLPWTFGGKTVEIKR 131
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; RESULT 5
US-10-234-671-100
; Sequence 100, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;               Wells, James A.
;               Presta, Leonard G.
;               Lowman, Henry B.
;               Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056.160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-056-160B-15

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Query Match          92.5%; Score 531; DB 9; Length 107;
Best Local Similarity 92.5%; Pred. No. 7.6e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIFYSNLSHGVS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIFYSNLSHGVS 60
Qy 61 RFSGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGGTKVEIK 107
Db 61 RFSGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGGTKVEIK 107

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RESULT 9

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US-10-234-671-15
; Sequence 15, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160

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; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
; US-10-234-671-15

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Query Match          92.5%; Score 531; DB 14; Length 107;
Best Local Similarity 92.5%; Pred. No. 7.6e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIFYSNLSHGVS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIFYSNLSHGVS 60
Qy 61 RFSGSGSGTDYTLTISSLPEDFATYYCQYSKLPWTFGGTVK 107
Db 61 RFSGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGGTKVEIK 107

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RESULT 10

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US-10-974-591-15
; Sequence 15, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-Nov-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093PID1C1
; TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-974-591-15

Query Match          92.5%; Score 531; DB 17; Length 107;
Best Local Similarity 92.5%; Pred. No. 7.6e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFSGGSGGTDYTLTISSLPEDFATYYCHQYSKLPWTFQGGTKVEIK 107
DB 61 RFSGGSGGTDYTLTISSLPEDFATYYCHQYSKLPWTFQGGTKVEIK 107

RESULT 11
US-09-056-160B-105
; Sequence 105, Application US/09056160B
; Patent No. US2002003231SAI
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-Aug-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-105

Query Match          92.3%; Score 530; DB 9; Length 110;
Best Local Similarity 90.7%; Pred. No. 9.4e-37;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
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;
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-974-591-15

Query Match          92.5%; Score 531; DB 17; Length 107;
Best Local Similarity 92.5%; Pred. No. 7.6e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFSGGSGGTDYTLTISSLPEDFATYYCHQYSKLPWTFQGGTKVEIK 108
DB 61 RFSGGSGGTDYTLTISSLPEDFATYYCHQYSKLPWTFQGGTKVEIK 108

RESULT 12
US-10-234-671-103
; Sequence 103, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-Apr-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-Apr-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-Aug-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-234-671-103

Query Match          92.3%; Score 530; DB 14; Length 110;
Best Local Similarity 90.7%; Pred. No. 9.4e-37;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFSGGSGGTDYTLTISSLPEDFATYYCHQYSKLPWTFQGGTKVEIK 108
DB 61 RFSGGSGGTDYTLTISSLPEDFATYYCHQYSKLPWTFQGGTKVEIK 108

RESULT 13
US-10-974-591-103
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.11574 Seconds
(without alignments)
1699.125 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DQMTQSPSSLSASVGRVT.....HOYSKLPWTFGGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	496	86.4	108	1 K1HUAU	Ig kappa chain V-I
2	488	85.0	127	2 S40367	Ig kappa chain V-J
3	472	82.2	108	1 K1HURE	Ig kappa chain V-I
4	471	82.1	125	2 S40333	Ig kappa chain V-J
5	469	81.7	129	2 S52789	Ig kappa chain V-I
6	468	81.5	123	2 S40331	Ig kappa chain - h
7	467	81.4	108	2 B49047	Ig kappa chain V-I
8	466	81.2	110	2 S41118	Ig kappa chain V-J
9	466	81.2	111	2 A38740	Ig kappa chain V-I
10	465	81.0	108	2 S44122	Ig kappa chain V-I
11	464	80.8	111	2 E38740	Ig kappa chain V-I
12	461	80.3	108	2 I39154	Ig kappa chain (BR
13	461	80.3	109	2 S31998	Ig kappa chain - h
14	460	80.1	107	2 S36264	Ig kappa chain V
15	459	80.0	108	1 K1HWE	Ig kappa chain V-I
16	459	80.0	111	2 G38740	Ig kappa chain V-I
17	459	80.0	139	2 S40365	Ig kappa chain - h
18	458	79.8	131	2 S40352	Ig kappa chain V-J
19	457	79.6	129	2 S40369	Ig kappa chain - h
20	456	79.4	111	2 C38740	Ig kappa chain V-I
21	455	79.3	108	2 S19674	Ig kappa chain V-I
22	455	79.3	141	2 A49134	Ig kappa chain V-I
23	454	79.1	108	1 K1HURY	Ig kappa chain V-I
24	453.5	79.0	107	2 S36275	Ig kappa chain V-I
25	453	78.9	107	2 B49026	Ig kappa chain V-I
26	453	78.9	108	1 K1HUG	Ig kappa chain V-I
27	453	78.9	109	2 S31981	Ig kappa chain - h
28	452.5	78.8	124	2 S40336	Ig kappa chain V-J
29	451	78.6	135	2 S24320	Ig kappa chain pre

30	450	78.4	108	1 K1HUUH	Ig kappa chain V-I
31	449.5	78.3	106	1 KC2397	anti-tetanus toxin
32	448	78.0	108	1 KWS73	Ig kappa chain V-I
33	447	77.9	117	2 S46371	Ig kappa chain V-J
34	446	77.7	108	1 K1HUKA	Ig kappa chain V-I
35	446	77.7	125	2 S40349	Ig kappa chain V-J
36	445.5	77.6	125	2 S40315	Ig kappa chain - h
37	445	77.5	108	1 K1HUBN	Ig kappa chain V-I
38	445	77.5	108	1 K1HULY	Ig kappa chain V-I
39	445	77.5	122	2 S40370	Ig kappa chain - h
40	445	77.5	129	2 S52793	Ig kappa chain V-I
41	445	77.5	132	2 S40334	Ig kappa chain - h
42	444	77.4	108	2 S47182	Ig kappa chain - h
43	444	77.4	117	2 S46376	Ig kappa chain V-J
44	444	77.4	122	2 S40314	Ig kappa chain - h
45	443	77.2	108	1 K1HUBI	Ig kappa chain V-I
46	443	77.2	129	2 S40317	Ig kappa chain - h
47	442	77.0	108	1 K1HUUU	Ig kappa chain V-I
48	442	77.0	120	2 S46370	Ig kappa chain V-J
49	442	77.0	129	1 K1HUKW	Ig kappa chain pre
50	442	77.0	130	2 S40368	Ig kappa chain - h
51	441	76.8	108	2 S69900	Ig kappa chain (cl
52	441	76.8	126	2 S40335	Ig kappa chain V-J
53	441	76.8	128	2 S46372	Ig lighc chain var
54	440	76.7	107	2 S36269	Ig lambda chain V
55	439	76.5	107	2 JL0139	Ig kappa chain V-I
56	439	76.5	107	2 I69017	anti-Hiv1 envelope
57	439	76.5	124	2 S40318	Ig kappa chain V-I
58	438	76.3	108	1 K1HUGL	Ig kappa chain V-I
59	437	76.1	108	1 K1HUDE	Ig kappa chain V-I
60	437	76.1	125	2 S40316	Ig kappa chain - h
61	436	76.0	108	1 K1HUSW	Ig kappa chain V-I
62	436	76.0	109	2 S31978	Ig kappa chain - h
63	436	76.0	129	2 S52792	Ig kappa chain V-I
64	436	76.0	132	2 S38646	Ig kappa chain V-I
65	435	75.8	123	2 S40313	Ig kappa chain V-J
66	435	75.8	125	2 S40350	Ig kappa chain - h
67	434.5	75.7	107	1 K1HUAR	Ig kappa chain V-I
68	434	75.6	107	2 S36262	Ig lambda chain V
69	434	75.6	117	2 S42263	Ig kappa chain V-I
70	434	75.6	117	2 S43528	Ig kappa chain V-I
71	434	75.6	122	2 A29380	Ig kappa chain pre
72	434	75.6	125	2 S40353	Ig kappa chain V-J
73	433	75.4	108	1 K1HUKU	Ig kappa chain V-I
74	433	75.4	109	2 S31979	Ig kappa chain - h
75	432	75.3	108	1 K1HUMS	Ig kappa chain V-I
76	432	75.3	108	2 S69903	Ig kappa chain (cl
77	432	75.3	115	2 JL0080	Ig kappa chain pre
78	431.5	75.2	109	1 K1HUMV	Ig kappa chain V-I
79	430	74.9	108	2 S36279	Ig lambda chain V
80	429	74.7	109	2 S31980	Ig kappa chain - h
81	428	74.6	95	2 PH0862	Ig kappa chain V-I
82	428	74.6	108	1 KWSAR	Ig kappa chain V-I
83	428	74.6	108	2 S31977	Ig kappa chain - h
84	427.5	74.5	108	2 S30521	Ig kappa chain V-I
85	427	74.4	95	2 PH0864	Ig kappa chain V-I
86	427	74.4	107	2 A48677	Ig kappa chain V-J
87	427	74.4	108	2 S69902	Ig kappa chain (cl
88	427	74.4	109	2 PH0888	Ig kappa chain V-I
89	427	74.4	110	2 PN0535	Ig kappa chain V-I
90	427	74.4	126	2 A34904	Ig kappa chain pre
91	427	74.4	127	2 S11240	Ig kappa chain V-I
92	426	74.2	108	1 K1HUEU	Ig kappa chain V-I
93	426	74.2	109	2 S32001	Ig kappa chain - h
94	426	74.2	124	2 S40348	Ig kappa chain V-J
95	425.5	74.1	107	2 S47183	Ig kappa chain - h
96	425	74.0	108	2 S36277	Ig lambda chain V
97	424	73.9	107	2 B48677	Ig kappa chain V-J
98	424	73.9	128	2 A26406	Ig kappa chain V-I
99	423.5	73.8	107	2 S69901	Ig kappa chain (cl
100	423.5	73.8	108	2 S34007	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

KIHUAD
Ig kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: A91653; A01862; S02573
R:Schleichl, H.; Hilsechmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653

A:Molecule type: protein
A:Residues: 1-108 <SCH>
A:Cross-references: UNIPROT:P01594
A:Note: the C region of this chain has the Inv (3) marker
R:Pehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Strei
Biophys. Struct. Mech. 1, 139-146, 1975
A:Title: The structure determination of the variable portion of the Bence-Jones protein
A:Reference number: A90729; MUID:77022433; PMID:1234024
A:Contents: annotation; X-ray crystallography
A:Note: the structure of the V region was determined by molecular replacement methods us
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A:Reference number: S02572; MUID:88005152; PMID:3115931
A:Contents: annotation
C:Comment: This is a Bence Jones protein.

C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 86.4%; Score 496; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 5.5e-37;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPS 60

DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIYDASNLSESGVPS 60

QY 61 RPSGGSGTDYTLTISSLOPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

DB 61 RPSGGSGAHFTFTISSLOPEDIATYYCQYDYLPWTFGQGTKEIKR 108

RESULT 2

S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 488; DB 2; Length 127;
Best Local Similarity 86.1%; Pred. No. 3.3e-36;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPS 60

DB 18 DIQMTQSPSSLSASVGDRTVITCRASQDISNYLNWYQKPGKAPKLLIYAASLSQSGVPS 77

QY 61 RPSGGSGTDYTLTISSLOPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

DB 78 RPSGGSGTDFTLTITSSLOPEDFATYYCQSYNTPTWTFQGTKEIKR 125

RESULT 3

KIHURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C:Accession: A91663; A01873
R:Palm, W.; Hilsechmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975

A:Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom ka

vollstaendige Aminosaeuresequenz des Proteins.

A:Reference number: A91663; MUID:76023758; PMID:809329

A:Accession: A91663

A:Molecule type: protein

A:Residues: 1-108 <PAL>

A:Cross-references: UNIPROT:P01607

A:Note: the C region of this chain has the Inv (1,2) marker

R:Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.

Biochemistry 14, 4943-4952, 1975

A:Title: The molecular structure of a dimer composed of the variable portions of the Benc

A:Reference number: A90392; MUID:76039968; PMID:1182131

A:Contents: annotation; X-ray crystallography, 2.0 angstroms

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-90/Domain: immunoglobulin homology <IMM>

F:23-88/Disulfide bonds: #status experimental

Query Match 82.2%; Score 472; DB 1; Length 108;

Best Local Similarity 82.4%; Pred. No. 7.2e-35;

Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPS 60

DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDIIRKYLNNWYQTPPGKAPKLLIYEASNLQAGVPS 60

QY 61 RPSGGSGTDYTLTISSLOPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

DB 61 RPSGGSGTDYTLTISSLOPEDIATYYCQYQSLPYTFGQGTKEIKR 108

RESULT 4

S40333

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40333

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40333

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 82.18; Score 471; DB 2; Length 125;
Best Local Similarity 82.2%; Pred. No. 1e-34;
Matches 88; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60
DB 19 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYKASSLESQVPS 78
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIK 107
DB 79 RFGSGSGTFTLTISLPDPDPATYVCCQYNSYPWTFGGTKVEIK 125

RESULT 5

S52789
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
R;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 469; DB 2; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.6e-34;
Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60
DB 23 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIHAASLETGVP 82
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIK 107
DB 83 RFGSGSGTFTLTISLPDPDPATYVCCQYDNLPLTFGGTKVEIK 129

RESULT 6

S40331
IG kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40331
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40331; MUID:94080891; PMID:8258341
A;Accession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <LE>
A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 468; DB 2; Length 123;
Best Local Similarity 85.0%; Pred. No. 1.8e-34;
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60
DB 17 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPS 76
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIK 107
DB 77 RFGSGSGTFTLTISLPDPDPATYVCCQYNSYPWTFGGTKVEIK 123

RESULT 7

B49047
IG kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 467; DB 2; Length 108;
Best Local Similarity 84.3%; Pred. No. 2e-34;
Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPS 60
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIK 108
DB 61 RFGSGSGTFTLTISLPDPDPATYVCCQYNSYPWTFGGTKVEIK 108

RESULT 8

S44118
IG kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44118
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re-
A;Reference number: S44105
A;Accession: S44118
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <HAW>
A;Cross-references: EMBL:X31395; NID:g472972; PIDN:CAA83270.1; PID:g940529
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 466; DB 2; Length 110;
Best Local Similarity 82.7%; Pred. No. 2.5e-34;
Matches 91; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKLLIYDASNLGTGVP 60
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKLP--WTFGGTKVEIK 108
DB 61 RFGSGSGTFTLTISLPDPDPATYVCCQYDNLPGVTFPGTKVDIKR 110

```
RESULT 9
A38740
Ig kappa chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: A38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: A38740
A:Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 466; DB 2; Length 111;
Best Local Similarity 79.6%; Pred. No. 2.5e-34;
Matches 86; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 4 DVQMTQTSSLSASLGDRVTITCSASQGISNYLNWYQKPGDGTVKLLIYVTSLSHSGVPS 63
QY 61 RPSGGSGGTDYTLTITSSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 64 RPSGGSGGTDYTLTISNLEPEDVATYCCQYQYKVPWTFGGKLEIKR 111

RESULT 10
S44122
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable r
A:Reference number: S44105
A:Accession: S44122
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAW>
A:Cross-references: EMBL:Z31390; NID:G472976; PIDN:CAA83265.1; PID:G940533
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.0%; Score 465; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 3e-34;
Matches 90; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKLGKAPKLLIYSASSLSQSGVPS 60
QY 61 RPSGGSGGTDYTLTITSSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 61 TFSGGSGGTDYTLTITSSLOPEDFATYCCQYQYKVPWTFGGKLEIKR 108

RESULT 11
E38740
Ig kappa chain V region (Py54) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: E38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
```

```
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: E38740
A:Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      80.8%; Score 464; DB 2; Length 111;
Best Local Similarity 79.6%; Pred. No. 3.7e-34;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 4 DVQMTQTSSLSASLGDRVTITCSASQGISNYLNWYQKPGDGTVKLLIYVTSLSHSGVPS 63
QY 61 RPSGGSGGTDYTLTITSSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 64 RPSGGSGGTDYTLTISDLEPDATYCCQYQYKVPWTFGGKLEIKR 111

RESULT 12
I39154
Ig kappa chain (BRE) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C:Accession: I39154
R:Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A:Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A:Reference number: I39154; MUID:96003804; PMID:7568160
A:Accession: I39154
A:Status: Preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-108 <RES>
A:Cross-references: EMBL:U31344; NID:G944925; PIDN:AAA79238.1; PID:G944926
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.3%; Score 461; DB 2; Length 108;
Best Local Similarity 82.4%; Pred. No. 6.7e-34;
Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISDYLIWYQKLGKAPNLLIYDASTLTSTGVPS 60
QY 61 RPSGGSGGTDYTLTITSSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 61 RPSGGSGGTEYTFITSSILQPDATYCCQYQYKVPWTFGGKLEIKR 108

RESULT 13
S31998
Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S31998
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31998
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 28.0249 Seconds
(without alignments)
1973.408 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSSLSASVGDRVT.....HOYSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	496	86.4	108	1	KV1B_HUMAN
2	472	82.2	108	1	KV1O_HUMAN
3	471	82.1	108	2	Q9UL77
4	465	81.0	236	2	Q6GMW1
5	459.5	80.1	107	2	Q96SA9
6	459	80.0	108	1	KV1R_HUMAN
7	456	79.4	236	2	Q723Y4
8	454	79.1	108	1	KV1P_HUMAN
9	453	78.9	108	1	KV1A_HUMAN
10	452	78.7	108	2	Q6GMX8
11	452	78.7	108	1	KV1Y_HUMAN
12	450	78.4	108	1	KV1H_HUMAN
13	450	78.4	108	2	Q9UL70
14	449	78.2	236	2	Q6GMX0
15	448	78.0	108	1	KV5J_MOUSE
16	448	78.0	236	2	Q6GMX9
17	446	77.7	108	1	KV1K_HUMAN
18	445	77.5	108	1	KV1M_HUMAN
19	445	77.5	108	1	KV1W_HUMAN
20	443	77.2	108	1	KV1C_HUMAN
21	442.5	77.1	107	2	Q9UL81
22	442	77.0	108	1	KV1N_HUMAN
23	442	77.0	116	2	Q96PF6
24	442	77.0	129	1	KV1W_HUMAN
25	440	76.7	236	2	Q6PIH7
26	439	76.5	244	2	Q65ZC8
27	438	76.3	108	1	KV1G_HUMAN
28	437	76.1	108	1	KV1E_HUMAN
29	437	76.1	234	2	Q7Z473
30	436	76.0	108	1	KV1Q_HUMAN
31	434.5	75.7	107	1	KV1D_HUMAN

ALIGNMENTS

32	434	75.6	240	2	Q65ZC9	Q65ZC9 homo sapien
33	433	75.4	108	1	KV1L_HUMAN	P01604 homo sapien
34	432	75.3	108	1	KV1S_HUMAN	P01611 homo sapien
35	431.5	75.2	109	1	KV1T_HUMAN	P01612 homo sapien
36	429	74.7	108	2	Q9UL79	Q9UL79 homo sapien
37	428	74.6	108	1	KV5K_MOUSE	P01644 mus musculus
38	427	74.4	108	1	KV5L_MOUSE	P01645 mus musculus
39	427	74.4	108	1	KV5M_MOUSE	P01646 mus musculus
40	426	74.2	108	1	KV1F_HUMAN	P01598 homo sapien
41	425	74.0	108	1	KV5O_MOUSE	P01648 mus musculus
42	423	73.7	108	1	KV5N_MOUSE	P01647 mus musculus
43	420	73.2	236	2	Q6PIH4	Q6PIH4 homo sapien
44	420	73.2	236	2	Q6PIH5	Q6PIH5 homo sapien
45	417	72.6	108	1	KV5U_MOUSE	Q9J946 mus musculus
46	416	72.5	107	2	Q9JL84	Q9JL84 mus musculus
47	414	72.1	129	1	KV1X_HUMAN	P04332 homo sapien
48	409	71.3	134	1	KV4C_HUMAN	P06314 homo sapien
49	400	69.7	108	1	KV5S_MOUSE	P01652 mus musculus
50	399	69.5	109	2	Q920E6	Q920E6 mus musculus
51	397	69.2	117	1	KV1J_HUMAN	P01602 homo sapien
52	395	68.8	236	2	Q7TS98	Q7TS98 mus musculus
53	394	68.6	117	1	KV1I_HUMAN	P01601 homo sapien
54	391	68.1	108	1	KV5Q_MOUSE	P01650 mus musculus
55	391	68.1	112	1	KV1U_HUMAN	P01613 homo sapien
56	388.5	67.7	129	1	KV3M_HUMAN	P18336 homo sapien
57	387	67.4	114	1	KV4A_HUMAN	P01625 homo sapien
58	386	67.2	108	1	KV5P_MOUSE	P01649 mus musculus
59	385	67.1	108	1	KV5T_MOUSE	P01653 mus musculus
60	384	66.9	128	1	KV5E_MOUSE	P01637 mus musculus
61	383	66.7	298	2	Q9QTF0	Q9QTF0 synthetic c
62	381.5	66.5	109	1	KV3D_HUMAN	P01622 homo sapien
63	381	66.4	130	1	KV5G_MOUSE	P01639 mus musculus
64	380	66.2	108	1	KV5R_MOUSE	P01651 mus musculus
65	379.5	66.1	109	1	KV3B_HUMAN	P01620 homo sapien
66	379.5	66.1	109	1	KV3E_HUMAN	P01623 homo sapien
67	379.5	66.1	129	1	KV3H_HUMAN	P04207 homo sapien
68	379.5	66.1	129	1	KV3L_HUMAN	P18335 homo sapien
69	378.5	65.9	133	1	KV4B_HUMAN	P01633 homo sapien
70	377	65.7	108	1	KV5D_MOUSE	P01636 mus musculus
71	376.5	65.6	110	1	KV3P_MOUSE	P01668 mus musculus
72	376.5	65.6	243	2	Q7TQM2	Q7TQM2 mus musculus
73	375	65.3	111	1	KV3O_MOUSE	P01667 mus musculus
74	375	65.3	111	1	KV3Q_MOUSE	P01669 mus musculus
75	374.5	65.2	134	2	Q8VDD0	Q8VDD0 mus musculus
76	372	64.8	108	2	Q9UL83	Q9UL83 homo sapien
77	372	64.8	238	2	Q6GJS7	Q6GJS7 mus musculus
78	369.5	64.4	109	1	KV3F_HUMAN	P01624 homo sapien
79	369.5	64.4	112	2	Q8K1F3	Q8K1F3 mus musculus
80	366.5	63.9	109	2	Q9UL78	Q9UL78 homo sapien
81	365.5	63.7	235	2	Q6FJF2	Q6FJF2 homo sapien
82	365	63.6	111	1	KV3M_MOUSE	P01665 mus musculus
83	365	63.6	149	1	KV5A_MOUSE	P01633 mus musculus
84	364.5	63.5	114	2	Q8K1F1	Q8K1F1 mus musculus
85	364.5	63.5	235	2	Q6GMW0	Q6GMW0 homo sapien
86	363	63.0	108	2	Q8VJ30	Q8VJ30 mus musculus
87	361.5	63.0	112	2	Q8K1F2	Q8K1F2 mus musculus
88	361	62.9	111	1	KV3L_MOUSE	P01664 mus musculus
89	361	62.9	111	2	Q920E9	Q920E9 mus musculus
90	360.5	62.8	109	2	Q9UL85	Q9UL85 homo sapien
91	359	62.5	111	1	KV3N_MOUSE	P01666 mus musculus
92	357.5	62.3	108	1	KV3A_HUMAN	P01619 homo sapien
93	357	62.2	128	1	KV3K_HUMAN	P06311 homo sapien
94	357	62.2	487	2	Q65ZL2	Q65ZL2 mus sp. fv/
95	356	62.0	111	1	KV3R_MOUSE	P01670 mus musculus
96	356	62.0	111	1	KV3S_MOUSE	P01671 mus musculus
97	356	62.0	127	2	Q925S9	Q925S9 mus musculus
98	356	62.0	131	1	KV3I_MOUSE	P01661 mus musculus
99	355	61.8	136	1	KV5B_MOUSE	P01634 mus musculus
100	354	61.7	109	1	KV4D_HUMAN	P83593 homo sapien

```
RESULT 1
KV10 HUMAN
ID KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=72189444; PubMed=5028201;
RX Schiechl H., Hilschmann N.;
RA "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -!- MISCELLANEOUS: This C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; KIHUAV.
DR PDB; 1JVS; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT STRAND 1 23
FT TURN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT STRAND 4 5
FT STRAND 10 12
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT TURN 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
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FT NON TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6FB9 CRC64;
Query Match 86.4%; Score 496; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.9e-43;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGDRTVITCSASQDISYLNWYQQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQWTQSPSSLSASVGDRTVITCSASQDISYLNWYQQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFSGGGSGTDVLTITSSLPQDEFTYCHQYSKLPWTGQGTKEIKR 108
DB 61 RFSGGGSGAHTFTTSSLPQDEFTYCHQYQDYLPWTGQGTKEIKR 108
RESULT 2
KV10 HUMAN
ID KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; IAR2; X-ray; @=1-107.
DR PDB; 1BWW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT STRAND 24 34
FT TURN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
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FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188CE2A CRC64;

Query Match
Best Local Similarity 82.2%; Score 472; DB 1; Length 108;
Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
DB 1 DIQWTSPLSLASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYEASNLQAGVPS 60

QY 61 RFGSGSGTDYTLTISLQPEDPATYCHQYSKLPWTFGGTKVEIKR 108
DB 61 RFGSGSGTDYTLTISLQPEDPATYCHQYSKLPWTFGGTKLQITR 108

RESULT 3
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Spleen;
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; I8W.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 82.1%; Score 471; DB 2; Length 108;
Matches 89; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
DB 1 DIQWTSPLSLASVSGDRVTITCSASQDISNYLNWYQKPGKAPNLLIYAASSLQSGVPS 60
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QY 61 RFGSGSGTDYTLTISLQPEDPATYCHQYSKLPWTFGGTKVEIKR 108
DB 61 RFGSGSGTDYTLTISLQPEDPATYCHQYSKLPWTFGGTKVEIKR 108

RESULT 4
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zedberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match
Best Local Similarity 81.0%; Score 465; DB 2; Length 236;
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 IQWTSPLSLASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 61
DB 24 IQWTSPLSLASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIYAASSLQSGVPS 83

QY 62 RFGSGSGTDYTLTISLQPEDPATYCHQYSKLPWTFGGTKVEIKR 108
DB 62 RFGSGSGTDYTLTISLQPEDPATYCHQYSKLPWTFGGTKVEIKR 108
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Db      84  FSGSGGTDTLTITSSLPEDFATYCYCLQDYNYPWTFGGTKVEIKR 130
RESULT 5
Q96SA9          PRELIMINARY;      PRT;    107 AA.
AC  Q96SA9;
DT  01-DEC-2001 (TREMBlrel. 19, Created)
DT  01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT  01-WAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE  variable region (Fragment).
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98375993; PubMed=9712075;
RA  Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT  "Molecular analysis of polyreactive monoclonal antibodies from
RT  rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT  antibody V region genes.";
RL  J. Immunol. 161:2020-2031(1998).
DR  EMBL; U96396; AAB68785.1; -
DR  PIR; B49047; B49047.
DR  PIR; PH0867; PH0867.
DR  PIR; S16840; S16840.
DR  PIR; S31977; S31977.
DR  PIR; S34083; S34083.
DR  PIR; S34086; S34086.
DR  HSSP; P01607; LBWW.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
FT  NON_TER 1
FT  NON_TER 107
FT  NON_TER 107
SQ  SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match      80.1%; Score 459.5; DB 2; Length 107;
Best Local Similarity 85.3%; Pred. No. 1.1e-39;
Matches 93; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY  1  DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNMYQQKPGKAPKLLIFYSNLSHGVP 60
Db  1  DIQMTQSPSSLSASVGDRVTITCRASQIGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVP 60
QY  61  RFSGSGGTDTLTITSSLPEDFATYCHQ-YSKLPWTFGGTKVEIKR 108
Db  61  RFSGSGGTDTLTITSSLPEDFATYCYCQSYSTL--TFGGTKVEIKR 107

RESULT 6
KVLR_HUMAN          STANDARD;      PRT;    108 AA.
AC  F01610;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Ig kappa chain V-I region WEA.
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=83273707; PubMed=6410398;
RA  Goni F., Frangione B.;
RT  "Amino acid sequence of the Fv region of a human monoclonal IgM
RT  (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT  in Klebsiella polysaccharides K30 and K33.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

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CC  -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC  against 3,4-pyruvylated galactose and isolated from a patient with
CC  Waldenstrom's macroglobulinemia.
DR  PIR; A01876; KIHUME.
DR  HSSP; P80362; LWTL.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Direct protein sequencing; Immunoglobulin V region;
KW  Monoclonal antibody.
FT  DOMAIN 1 23
FT  DOMAIN 24 34
FT  DOMAIN 35 49
FT  DOMAIN 50 56
FT  DOMAIN 57 88
FT  DOMAIN 89 97
FT  DOMAIN 98 107
FT  DISULFID 23 88
FT  NON_TER 108
FT  NON_TER 108
SQ  SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match      80.0%; Score 459; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 1.2e-39;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY  1  DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNMYQQKPGKAPKLLIFYSNLSHGVP 60
Db  1  DIQMTQSPSSLSASVGDRVTITCRASQIGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVP 60
QY  61  RFSGSGGTDTLTITSSLPEDFATYCHQYQSKLPWTFGGTKVEIKR 108
Db  61  RFSGSGGTDTLTITSSLPEDFATYCYCQSYSTL--TFGGTKVEIKR 108

RESULT 7
Q723Y4          PRELIMINARY;      PRT;    236 AA.
AC  Q723Y4;
DT  01-OCT-2003 (TREMBlrel. 25, Created)
DT  01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT  01-WAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Hypothetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Skeletal Muscle;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA  Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA  Bosak S.A., LeGall P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strauberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AA05332.1; -;
DR HSSP; P01834; 1HEZ.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_1.

SQ SEQUENCE 236 AA; 25702 MW; 7BFE4ED23084BC6 CRC64;
Query Match 79.4%; Score 456; DB 2; Length 236;
Best Local Similarity 81.5%; Pred. No. 6.3e-39;

Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFYSNNLHSGVPS 60
Db 23 DIQMTQSPSSLSASVGRVTITCRASQDISNYLAWFOQKPGKAPKSLIYGASSLQSGVQS 82

Qy 61 RFSGGSGTDYTLTISSLPEDPATYCHQYKLPWTFGGTKVEIKR 108
Db 83 KFSGSGGTDFTLTISLPEDPATYCCQYKSPVTFGGTKLEIKR 130

RESULT 8
KVLP_HUMAN STANDARD; PRT; 108 AA.

AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;

RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080 (1967).
RN [2]

RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hees M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;

RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
York (1969).

CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC PIR; A91638; KIHURY.

DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;

KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108

SQ SEQUENCE 108 AA; 11782 MW; PSACEDBSA313DF3A CRC64;
Query Match 79.1%; Score 454; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 4.1e-39;

Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFYSNNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISIFLNWYQOKPGKAPKLLIYDASKLEAGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPEDPATYCHQYKLPWTFGGTKVEIKR 108
Db 61 RFSGTSGTDFTLTISLPEDPATYCCQFDNLPLTFGGTKVDPR 108

RESULT 9
KVIA_HUMAN STANDARD; PRT; 108 AA.

AC P01533;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;

RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";

RL J. Biol. Chem. 244:3550-3560 (1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A01861; KIHUAG.
DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;

KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT NON TER 108 108

SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;
Query Match 78.9%; Score 453; DB 1; Length 108;
Best Local Similarity 79.6%; Pred. No. 5.2e-39;

Matches 86; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

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QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNMVYQKPGKAPKLLIFYSNLSHGVPVS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNMVYQKPGKAPKLLIYDASNLETGVPVS 60

QY 61 RFSGGSGTDTYLTITSSLOPEDFATYYCHQYKSLPMTFCQGTKEIKR 108
Db 61 RFSGGSGTDTYLTITSSLOPEDFATYYCHQYKSLPMTFCQGTKEIKR 108

RESULT 10
Q6GMX8
ID AC O6GMX8 PRELIMINARY; PRT; 236 AA.
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner K.H., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073764; AAH3764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 78.9%; Score 453; DB 2; Length 236;
Best Local Similarity 80.6%; Pred. No. 1.3e-38;
Matches 87; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNMVYQKPGKAPKLLIFYSNLSHGVPVS 60
Db 23 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNMVYQKPGKAPKLLIYDASNLETGVPVS 62
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QY 61 RFSGGSGTDTYLTITSSLOPEDFATYYCHQYKSLPMTFCQGTKEIKR 108
Db 83 RFSGGSGTDTYLTITSSLOPEDFATYYCHQYKSLPMTFCQGTKEIKR 130

RESULT 11
KVLY_HUMAN
ID AC KVLY_HUMAN STANDARD; PRT; 108 AA.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-L region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
related fragment of the human KI Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1WTL; X-ray; A/B=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT CONFLICT 30 31
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT TURN 33 38
FT STRAND 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
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FT STRAND 98 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 78.7%; Score 452; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 6.6e-39;
Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTSFSSLSASVGRDVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLIHSGVPS 60
DB 1 DIQWTSFSSLSASVGRDVTITCRASQDITNYVMVFQRFQAPKVLIIYGASILETGVP 60
QY 61 RFSGSGSGTDYTLTISSQLQPEDFATYYCHQYSKLPWTFGGQTKVEIKR 108
DB 61 RFSGSGSGTDFTFTISSLQPEDATYYCQYDTLPLTFGGGTKVDIKR 108

RESULT 12
KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-1 region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hillechmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RC Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; KIHUHU.
DR PDB; 1P6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 34 Framework-1.
FT DOMAIN 35 49 Complementarity-determining-1.
FT DOMAIN 50 56 Framework-2.
FT DOMAIN 57 88 Complementarity-determining-2.
FT DOMAIN 89 97 Framework-3.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON TER 108 By similarity.
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 78.4%; Score 450; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 1.1e-39;
Matches 87; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQWTSFSSLSASVGRDVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLIHSGVPS 60
DB 1 DIQWTSFSSLSASVGRDVTITCRASQDISNLYSWYQOKPGKAPQVLIYAASSLP 60
QY 61 RFSGSGSGTDYTLTISSQLQPEDFATYYCHQYSKLPWTFGGQTKVEIKR 108

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Dd 61 RFSGSGGTDFTLTISSLPEDFATYYCQNYITPTSFQGTRVEIKR 108

RESULT 13
Q9UL70 PRELIMINARY; PRT; 108 AA.

ID Q9UL70 AC Q9UL70 DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RW Xu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL ENBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSP; P01607; 1BW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM04008; IGV; I.
DR PROSITE; PS0835; IG LIKE; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 78.4%; Score 450; DB 2; Length 108;
Best Local Similarity 80.6%; Pred. No. 1.le-38;
Matches 87; Conservative 6; Mismatches 15; Indels 0; G

QY 1 DIQMTPSSLSASVGRVTITCSAQDTSNLYNWYQQKPGKAPKLLIFYSNLHS
Db 1 DIQMTPSSLSASVGRVTITCRASQISNLYAWYQQKPGKVPKSLIYAASTLOS
QY 61 RFSGSGGTDFTLTISSLPEDFATYYCHQYSKLPWTFCGGTKVEIKR 108
Db 61 RFSGSGGTDFTLTISSLPEDVATYYCQKNSAPRTFGPGTKLEIKR 108

RESULT 14
ID Q6GMX0 PRELIMINARY; PRT; 236 AA.

ID Q6GMX0 AC Q6GMX0 DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=Spleen.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausner R.B., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.R., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 175.288 Seconds
(without alignments)
1284.140 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVQLVSGGDFVPGGSLRV.....IVEFLNRWTFQCSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3071	100.0	582	4	AAB81987
2	3026	98.5	582	4	AAB81991
3	2780.5	90.5	583	4	AAB83156
4	2760.5	89.9	581	4	AAB81972
5	2750.5	89.6	579	6	AAB83444
6	2750.5	89.6	579	6	AAO30910
7	2719.5	88.6	575	8	ADP42961
8	2621	85.3	580	6	AAO30915
9	2589	84.3	580	6	AAO30913
10	2247	73.2	449	8	ADR23346
11	2246.5	73.2	447	6	AAE33522
12	2240.5	73.0	447	6	AAE33523
13	2238.5	72.9	449	5	AAO18400
14	2238.5	72.9	697	8	ADQ07403
15	2238.5	72.9	697	8	ADQ07403
16	2238.5	72.9	701	8	ADQ07409
17	2238.5	72.9	701	8	ADQ12186
18	2236.5	72.8	447	6	AAE33524
19	2236.5	72.8	450	8	ADH34587
20	2234.5	72.8	445	6	AAO31101
21	2233	72.7	449	6	ABP58273
22	2233	72.7	468	6	ABP58275
23	2232	72.7	451	8	ADH34584
24	2231.5	72.7	444	6	AAE35327
25	2231.5	72.7	444	6	AAE34876

99 2167 70.6 451 2 AA955661 Mus muscu
100 2167 70.6 451 3 AA85201 Light cha

ALIGNMENTS

RESULT 1
AAB81987
ID AAB81987 standard; protein; 582 AA.
XX
AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 41; Page 168-172; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;
Query Match 100.0%; Score 3071; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.3e-153;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGDFVQPGGSLRVSCAAGFAPFAMSWVRQAPGKGLEWVAYISGGSGGTYY 60
DB 1 EVQLVESGGDFVQPGGSLRVSCAAGFAPFAMSWVRQAPGKGLEWVAYISGGSGGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYVFDSWGQGLTLTVSSA 120
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYVFDSWGQGLTLTVSSA 120
QY 121 STKGSPVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
DB 121 STKGSPVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
QY 181 LYSLSVTVTPSSSLGTQTYIICNVNHPKNTKVDKKVEPKSCDKTHCTCPCPAPÉLGGP 240
DB 181 LYSLSVTVTPSSSLGTQTYIICNVNHPKNTKVDKKVEPKSCDKTHCTCPCPAPÉLGGP 240
QY 241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Db 241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
QY 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420
Db 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420
QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINNY 480
Db 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINNY 480
QY 481 KNPKLTRMLTFKYPMPKATELKHLCLEELKPLEEVLNLAQSNFHLRPRDLISINNV 540
Db 481 KNPKLTRMLTFKYPMPKATELKHLCLEELKPLEEVLNLAQSNFHLRPRDLISINNV 540
QY 541 IVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 582
Db 541 IVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 582

RESULT 2
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;
Query Match 98.5%; Score 3026; DB 4; Length 582;
Best Local Similarity 98.3%; Pred. No. 5.2e-151;
Matches 572; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSPHYAMSVWRQAPKGLEWVAYISSGGSTYY 60
Db 1 EVTLVESGGDFVQPGGSLKVSCAASGFAFSPHYAMSVWRQTPAKRLEWVAYISSGGSTYY 60
QY 61 SDSVKGRTTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYYPDSWGQGLTLYVSSA 120
Db 61 SDSVKGRTTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYYPDSWGQGLTLYVSSA 120
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180
Db 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180
QY 181 LYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELLGGP 240
Db 181 LYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELLGGP 240
QY 241 SVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNS 300
Db 241 SVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNS 300
QY 301 TYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPGRDEL 360
Db 301 TYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPGRDEL 360
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420
Db 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420
QY 421 QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGINNY 480
Db 421 QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGINNY 480
QY 481 KNPKLTRMLTFFKYPMPKATLKHLCLEBELKPLEEVNLNLAQSKNPHLRPRDLISNINV 540
Db 481 KNPKLTRMLTFFKYPMPKATLKHLCLEBELKPLEEVNLNLAQSKNPHLRPRDLISNINV 540
QY 541 IVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 582
Db 541 IVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 582

RESULT 3
AAB83156 ID AAB83156 standard; protein; 583 AA.
XX AC AAB83156;
XX DT 02-JUL-2001 (first entry)
XX Ganglioside GM2 antibody-related protein #1.
XX Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
XX Unidentified.
XX OS
XX PN WO200123431-A1.
XX PD 05-APR-2001.
XX 29-SEP-2000; 2000WO-JP006775.
XX 30-SEP-1999; 99JP-00278292.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Hanai N, Nakamura K, Niwa R;
XX WPI; 2001-266142/27.
XX Monoclonal antibodies against ganglioside GM2 combined with drugs,
XX radioisotopes or proteins for treatment and diagnosis of cancer.
XX Claim 43; Page 61-65; 80pp; Japanese.

XX The present invention relates to derivatives of an antibody against
CC ganglioside GM2. The antibody may be a monoclonal antibody or its
CC fragments. The antibody is combined with a radioactive isotope, protein
CC or small drug in the treatment and diagnosis of cancer
XX Sequence 583 AA;
SQ Query Match 90.5%; Score 2780.5; DB 4; Length 583;
Best Local Similarity 89.9%; Pred. No. 4.1e-138;
Matches 526; Conservative 22; Mismatches 32; Indels 5; Gaps 2;
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSPHYAMSVWRQAPKGLEWVAYISSGGSTYY 60
Db 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNMDWVKQSPQGLEWVGYYIPNNGGTGY 60
QY 61 SDSVKGRTTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTY---PDSWGQGLTLY 117
Db 61 NQKFKSKVTITVDSTSTAYMELHLSRSEDVAYYC--ATYGHYYGYMFAYWGQGLTLY 118
QY 118 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177
Db 119 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQ 178
QY 178 SGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELL 237
Db 179 SGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELL 238
QY 238 GGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297
Db 239 GGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 298
QY 298 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 357
Db 299 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 358
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 417
Db 359 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 418
QY 418 RWOQGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGI 477
Db 419 RWOQGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGI 478
QY 478 NNYKNPKLTRMLTFFKYPMPKATLKHLCLEBELKPLEEVNLNLAQSKNPHLRPRDLISN 537
Db 479 NNYKNPKLTRMLTFFKYPMPKATLKHLCLEBELKPLEEVNLNLAQSKNPHLRPRDLISN 538
QY 538 INVIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 582
Db 539 INVIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 583

RESULT 4
AAB81972 ID AAB81972 standard; protein; 581 AA.
XX AC AAB81972;
XX DT 03-JUL-2001 (first entry)
XX Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
XX Ganglioside; GD2; complementation determining region; CDR; antibody;
XX mouse; cancer.
XX Synthetic.
XX OS
XX PN WO200123573-A1.
XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-JP006773.
XX PF

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XX 30-SEP-1999; 99JP-00278290.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Hansi N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266163/27.
XX Human type complementation-determining domain transplanted antibody and
XX derivatives against ganglioside GD2, useful in diagnosis and therapy of
XX e.g. tumors, has low antigenicity, little side effects but potent
XX activity in cancer.
XX
XX Example 3; Page 111-114; 123pp; Japanese.
XX
XX The present invention describes an antibody, which can react specifically
XX with ganglioside GD2, and is transplanted with a human type
XX complementation-determining domain (CDR), or its fragments. The antibody
XX and its derivatives are useful in diagnosis and therapy of tumours,
XX particularly cancer diagnosis. The present sequence is a protein used in
XX the exemplification of the invention
XX
XX Sequence 581 AA;
XX
Query Match 89.9%; Score 2760.5; DB 4; Length 581;
Best Local Similarity 90.0%; Pred. No. 4.6e-137;
Matches 524; Conservative 22; Mismatches 35; Indels 1; Gaps 1;
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAPFASHVAMSVROAPGKGLEWVAYISSGGSGTY 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 QVQLVESGGLVKPSQTLISITCVSGFSLASNIHWVQPPGKGLWIGVWAGGS-TNY 59
QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGLTLTVSSA 120
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
60 NSALMSRLTISKDNSKNQVFLKMSLTAADTAVYCAKESDDYSFAYWGQGLTLTVSSA 119
QY 121 STKGSPVFPPLAPSSKSTSGGTAALGCLVKDYPPPEPTVSNWNGALTSVHPTFPAVLQSG 180
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
120 STKGSPVFPPLAPSSKSTSGGTAALGCLVKDYPPPEPTVSNWNGALTSVHPTFPAVLQSG 179
QY 181 LYSLSVWTVPSSSLGTQYIICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
180 LYSLSVWTVPSSSLGTQYIICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 239
QY 241 SVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQNS 300
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
240 SVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQNS 299
QY 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
300 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 359
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 420
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 419
QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLDDLQMLINGINNY 480
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
420 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLDDLQMLINGINNY 479
QY 481 KNPKLTRMLTFFKYPKPKATLKHQCLLEEELKPLEEVNLAKSNFHLRPRDLISNINV 540
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
480 KNPKLTRMLTFFKYPKPKATLKHQCLLEEELKPLEEVNLAKSNFHLRPRDLISNINV 539
QY 541 IVLELKGSTTFMCEYADDTATVIFLNRIWITFCQSIISTLT 582
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
540 IVLELKGSTTFMCEYADDTATVIFLNRIWITFCQSIISTLT 581
```

RESULT 5
AAE33444

ID AAE33444 standard; protein; 579 AA.

```
XX AAE33444;
XX 02-APR-2003 (first entry)
XX KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
XX Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EPCAM;
XX cancer; gene therapy; interleukin-2; IL2; fusion protein.
XX Unidentified.
XX WO200290566-A2.
XX 14-NOV-2002.
XX 03-MAY-2002; 2002WO-US013844.
XX 03-MAY-2001; 2001US-0288564P.
XX (LEXI-) LEXIGEN PHARM CORP.
XX Gillies SD, Lo K, Qian X;
XX WPI; 2003-111985/10.
XX N-PSDB; AAD51139.
XX New recombinant anti-EpCAM antibody having an amino acid sequence
XX defining an immunoglobulin light or heavy chain framework region, useful
XX for the diagnosis, prognosis and treatment of cancer.
XX Disclosure; Page 80-82; 82pp; English.
XX
XX The present invention relates to novel recombinant anti-EpCAM (human
XX epithelial cell adhesion molecule) antibodies comprising an amino acid
XX sequence defining an immunoglobulin light or heavy chain framework
XX region. Sequences of the present invention are useful for the diagnosis,
XX prognosis and treatment of cancer. They are also used in gene therapy.
XX The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
XX fusion protein. This sequence is used to illustrate the method of the
XX invention
XX
XX Sequence 579 AA;
XX
Query Match 89.6%; Score 2750.5; DB 6; Length 579;
Best Local Similarity 88.5%; Pred. No. 1.5e-136;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAPFASHVAMSVROAPGKGLEWVAYISSGGSGTY 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 QIQLVQSGAEVKKPQGETVKISKASGYFTFYGMWVVKQTPCKGLKMWGWINTYTGEPTY 60
QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYTFYFDSWGQGLTLTVSS 119
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 ADPPKGFAPFASLETSTSTAFQINNLRSEDTATYFCVRFISKGDY---WGQGSTVTVSS 116
QY 120 ASTKGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSVHPTFPAVLQSS 179
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
117 ASTKGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSVHPTFPAVLQSS 176
QY 180 GLYSLSVVTVPSSSLGTQYIICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
177 GLYSLSVVTVPSSSLGTQYIICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 236
QY 240 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 299
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
237 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 296
QY 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
297 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 356
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
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Db 357 MTKNQSLTCLVGFYPSDIAVWESNGQENNYKTPPVLDSDGSFPLYSKLTVDKSRW 416
Qy 420 QQGNVFCSCVWHEALHNHYTKSLSPGKAPTSSSTKKTQLOLEHLLDLOMLNGINN 479
Db 417 QQGNVFCSCVWHEALHNHYTKSLSPGKAPTSSSTKKTQLOLEHLLDLOMLNGINN 476
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVLNLAQSKNFHLRPRDLISIN 539
Db 477 YKNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVLNLAQSKNFHLRPRDLISIN 536
Qy 540 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIIISTLT 582
Db 537 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIIISTLT 579

RESULT 6
AAO30910
ID AAO30910 standard; protein; 579 AA.
XX AC AAO30910;
XX AC
DT 22-SEP-2003 (first entry)
XX di-KS-ala-IL2 (D20T) variant protein.
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; fusion protein; human.
XX Homo sapiens.
OS Unidentified.
OS Chimeric.
PN WO2003048334-A2.
XX
XX 12-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US038780.
PR 04-DEC-2001; 2001US-0337113P.
PR 12-APR-2002; 2002US-0371966P.
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
PA
XX Gillies SD;
XX WPI; 2003-513757/48.
XX
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT moiety, useful for preparing a composition for treating cancer, viral
PT infections or immune disorders.
XX
XX Example 10; Page 60-63; 71pp; English.
XX
XX The invention relates to cytokine fusion proteins with increased
CC therapeutic index and methods for increasing the therapeutic index of
CC such fusion proteins. The fusion protein comprises a non-interleukin-2
CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC composition for treating cancer, viral infections or immune disorders.
CC The fusion protein is also used in gene therapy. The present sequence is
CC di-KS-ala-IL2 (D20T) variant protein comprising di-KS heavy chain fused
CC to human IL-2 (D20T) variant protein. This sequence is used to illustrate
CC the method of the invention
XX
XX Sequence 579 AA;
Query Match 89.6%; Score 2750.5; DB 6; Length 579;
Best Local Similarity 88.5%; Pred. No. 1.5e-136;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;
Qy 1 EVOLVESGGDFVPGGSLRVSCHAFSHYAMSWRQAPGKLEWVAYISSGGSGTY 60
Db 1 QIOLVQSGPELKKPGSSVKISKASGYTFTNYGMNVVRQAPGKLGKMGWINTYTGPTY 60

Qy 61 SDSVKGRFTISRDNSTLYLQMRSLRABDSAVYFCTR-VKLGTYYPDSWGQGTLLTVSS 119
Db 61 ADDFGKRFITAEATSTSLYLQNLNLRSEDATYFCVRPISKDY----WGQGTTVTVSS 116
Qy 120 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db 117 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176
Qy 180 GLYSLSVVTVSSSSLGTOYICNVNHKPSNTKVDKKVPRKPSCKDTHTCPPCPAPELGG 239
Db 177 GLYSLSVVTVSSSSLGTOYICNVNHKPSNTKVDKKVPRKPSCKDTHTCPPCPAPELGG 236
Qy 240 PSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRBEQYN 299
Db 237 PSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRBEQYN 296
Qy 300 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 359
Db 297 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 356
Qy 360 LTKNQVSLTCLVKGFYPSDIAVWESNGQENNYKTPPVLDSDGSFPLYSKLTVDKSRW 419
Db 357 MTKNQVSLTCLVKGFYPSDIAVWESNGQENNYKTPPVLDSDGSFPLYSKLTVDKSRW 416
Qy 420 QQGNVFCSCVWHEALHNHYTKSLSPGKAPTSSSTKKTQLOLEHLLDLOMLNGINN 479
Db 417 QQGNVFCSCVWHEALHNHYTKSATATPCAAPTSSSTKKTQLOLEHLLDLOMLNGINN 476
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVLNLAQSKNFHLRPRDLISIN 539
Db 477 YKNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVLNLAQSKNFHLRPRDLISIN 536
Qy 540 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIIISTLT 582
Db 537 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIIISTLT 579

RESULT 7
ADP42961
ID ADP42961 standard; protein; 575 AA.
XX AC ADP42961;
XX AC
DT 23-SEP-2004 (first entry)
XX
DE Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
XX immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
KW cancer; cell surface glycosphingolipid; IL-2.
XX
XX Synthetic.
XX
XX WO2004055056-A1.
PN
XX
XX 01-JUL-2004.
PD
XX
XX 16-DEC-2003; 2003WO-EP014295.
PF
XX
XX 17-DEC-2002; 2002US-0433945P.
PR
XX
PA (MERE) MERCK PATENT GMBH.
XX
XX Gillies SD, Lo K;
XX
XX WPI; 2004-488049/46.
DR
XX N-PSDB; ADP42959.
XX
PT New modified m14.18 antibodies with reduced immunogenicity and that
PT specifically bind the human cell surface glycosphingolipid GD2, useful
PT for treating cancer.
XX
XX Disclosure; SEQ ID NO 6; 51pp; English.
PS


```

Qy 540 VIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 582
Db 538 VIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 580

RESULT 9
AAO30913
ID AAO30913 standard; protein; 580 AA.
AC AAO30913;
DT 22-SEP-2003 (first entry)
DE di-NHS76 (gamma2h) (FN-AQ)-ala-IL2 (D20T) variant protein.
KW Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX WO2003048334-A2.
XX 12-JUN-2003.
XX 04-DEC-2002; 2002WO-US038780.
XX 04-DEC-2001; 2001US-0337113P.
XX 12-APR-2002; 2002US-0371966P.
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
XX Gillies SD;
XX WPI; 2003-513757/48.
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
XX moiety, useful for preparing a composition for treating cancer, viral
XX infections or immune disorders.
XX Claim 37; Page 64-67; 71pp; English.
XX The invention relates to cytokine fusion proteins with increased
XX therapeutic index and methods for increasing the therapeutic index of
XX such fusion proteins. The fusion protein comprises a non-interleukin-2
XX (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
XX composition for treating cancer, viral infections or immune disorders.
XX The fusion protein is also used in gene therapy. The present sequence is
XX di-NHS76 (gamma2h) (FN-AQ)-ala-IL2 (D20T) variant protein comprising di-
XX KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
XX is used to illustrate the method of the invention
XX Sequence 580 AA;

Query Match 84.3%; Score 2589; DB 6; Length 580;
Best Local Similarity 85.18; Pred. No. 4.6e-128;
Matches 497; Conservative 29; Mismatches 52; Indels 6; Gaps 5;

Qy 1 EVQLVESGGDFVPGGSLRVSRAASGFAFSH-YAMSWVRQAPGKLEWVAYISGGSGTY 59
Db 1 QVQLQESGGPLVKPSETLSLTCAVSGYSISSGYWGWIRQPPGKLEWIGSIYHSGS-TY 59

Qy 60 YSDSVKGRFTISRDNKNTLYLQWRSIARSDSAVYFCTRVLKLTYYTDSGQGTLLTVSS 119
Db 60 YNPSLKSRVTSVDTSKNQFSLKLSVTAADATVYYCARGKWSK--FDYWGQGTLLTVSS 117

Qy 120 -ASTKGPSVPLAPSRSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
Db 118 GASTKGPSVPLAPCSRSTSESTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 177

Qy 179 SGLYSLSVVTVFPSSSLGTQTYICNVNHPKPSNTKVDKVPKSCDKTHHTCPPCPAPP 238

```

CC library was shown to specifically recognise the human CD72 receptor. The
 CC scFv was recloned in IGG expression vector C01 using primers designed to
 CC restore complete human frameworks, thereby generating antibody 004. Such
 CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used
 CC as internalising human binding molecules of the invention. These
 CC internalising human binding molecules are capable of (specifically)
 CC binding to CD72 or its antigenic determinant, and preferably bind to CD72
 CC associated with cells. Upon binding to CD72 present on the surface of
 CC target cells, the binding molecules internalise. In addition to the
 CC internalising human binding molecules, the invention provides
 CC immunoconjugates comprising an internalising human binding molecule and a
 CC tag (toxic substance, radioactive substance, liposome and/or enzyme),
 CC nucleic acids encoding these, and compositions comprising them. The
 CC internalising human binding molecule, immunoconjugate, nucleic acid
 CC molecule or composition can be used in the diagnosis and/or treatment of
 CC cancer and B cell associated autoimmune disorder (claimed). An
 CC internalising human binding molecule comprising the present heavy chain
 CC sequence is specifically claimed.
 XX
 SQ Sequence 449 AA;

Query Match 73.2%; Score 2247; DB 8; Length 449;
 Best Local Similarity 94.0%; Pred. No. 3.3e-110;
 Matches 422; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGGSLRVSCAAGFAPFHYAMSWVRQAPGKLEWYVAYISGGSGTY 60
 DB 1 EVQLVESGGGLVQPGGSLRSCAAGFTFGYLMWVRQAPGKLEWYVAYISYDGSNKYY 60
 QY 61 SDSVKGRFTISRDNSKNTLYLQMSRLRAEDSAVYFCTRVKLGLTYFDNSWGQGTLLTVSSA 120
 DB 61 ADSVKGRFTISRDNSKNTLYLQMSRLRAEDTAVYCARARRDTNLFYWGQGTLLTVSSA 120
 QY 121 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180
 DB 121 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180
 QY 181 LYSLSVWTVTPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPPELLGGP 240
 DB 181 LYSLSVWTVTPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPPELLGGP 240
 QY 241 SVFLPPPKDKTLMTISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
 DB 241 SVFLPPPKDKTLMTISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
 QY 301 TYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
 DB 301 TYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEM 360
 QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420
 DB 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420
 QY 421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
 DB 421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449

RESULT 11
 AAE33522
 ID AAE33522 standard; protein; 447 AA.
 XX
 AC AAE33522;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human AQC2 heavy chain protein.
 XX
 KW Human; very late activation antigen; VLA-1; betal containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;

KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia.
 OS
 XX Homo sapiens.
 PN WO200283854-A2.
 XX 24-OCT-2002.
 PF 12-APR-2002; 2002WO-US011521.
 XX 13-APR-2001; 2001US-0283794P.
 PR 06-JUL-2001; 2001US-0303689P.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;
 XX
 DR WPI; 2003-093009/08.
 XX
 PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.
 PS Claim 6; Page 75; 248pp; English.
 XX
 CC The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; betal containing integrins) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury, is
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human AQC2 heavy chain protein
 XX
 SQ Sequence 447 AA;

Query Match 73.2%; Score 2246.5; DB 6; Length 447;
 Best Local Similarity 95.1%; Pred. No. 3.5e-110;
 Matches 426; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSCAAGFAPFHYAMSWVRQAPGKLEWYVAYISGGSGTY 60
 DB 1 EVQLVESGGGLVQPGGSLRSCAAGFTFSRYTMSWVRQAPGKLEWYVATISGGGH-TTY 59
 QY 61 SDSVKGRFTISRDNSKNTLYLQMSRLRAEDSAVYFCTRVKLGLTYFDNSWGQGTLLTVSSA 120
 DB 60 LDSVKGRFTISRDNSKNTLYLQMSRLRAEDTAVYCTRGFGDGYFDVWGQGTLLTVSSA 119
 QY 121 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180
 DB 120 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 179

QY 181 LYSLSVVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 240
 |||||
 Db 180 LYSLSVVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 239
 |||||
 QY 241 SVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 300
 |||||
 Db 240 SVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 299
 |||||
 QY 301 TYRVVSVLTVLHODWLNKGKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
 |||||
 Db 300 TYRVVSVLTVLHODWLNKGKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359
 |||||
 QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 420
 |||||
 Db 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 419
 |||||
 QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448
 |||||
 Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447

RESULT 12

AAE33523
 ID AAE33523 standard; protein; 447 AA.

AC AAE33523;

DT 02-APR-2003 (first entry)

XX Human AQC2 heavy chain mutant protein, haaQC2.

XX Human; very late activation antigen; VLA-1; betal containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia; mutant; mutein.

XX Homo sapiens.

XX WO200283854-A2.

XX 24-OCT-2002.

XX 12-APR-2002; 2002WO-US011521.

XX 13-APR-2001; 2001US-0283794P.

XX 06-JUL-2001; 2001US-0303689P.

XX (BIOJ) BIOGEN INC.

XX Lyne PD, Garber EA, Saldanha JW, Karpueas M;

XX WPI; 2003-093009/08.

XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.

XX Example 23; Page 91-92; 248pp; English.

XX The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; betal containing integrins) antigens and
 CC methods of using these antibodies to treat immunological disorders. The

CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC psoriasis (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC parietaritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human AQC2 heavy chain mutant protein, haaQC2
 XX

XX Sequence 447 AA;

Query Match 73.0%; Score 2240.5; DB 6; Length 447;

Best Local Similarity 94.9%; Pred. No. 7.2e-110;

Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAPFSHVAMSVVROAPGKLEWAVYISSGGSGTY 60

|||||

Db 1 EVOLVESGGGLVQPGGSLRVSCAASGFTFSRYTMSVVRQAPGKLEWAVATISGGGH-TYY 59

|||||

QY 61 SDSVKGRTISRDNKNTLYLQWNSLRABDSAVYFCTRVKLGTYTFDSMGQGLLTVSSA 120

|||||

Db 60 LDSVKGRTISRDNKNTLYLQWNSLRABDTAVYCTRGDGGYFDVWQGLTAVTSSA 119

|||||

QY 121 STKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 180

|||||

Db 120 STKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 179

|||||

QY 181 LYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 240

|||||

Db 180 LYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 239

|||||

QY 241 SVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 300

|||||

Db 240 SVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 299

|||||

QY 301 TYRVVSVLTVLHODWLNKGKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

|||||

Db 300 TYRVVSVLTVLHODWLNKGKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

|||||

QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 420

|||||

Db 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 419

|||||

QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448

|||||

Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447

|||||

RESULT 13

AAO18400

ID AAO18400 standard; protein; 449 AA.

XX AAO18400;

XX 11-OCT-2002 (first entry)

DE Mature humanised murine CBE11 heavy chain variable domain.

KW Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;
 KW neoplasia; LT-beta-R; light chain; heavy chain; variable region.

XX Mus sp.

OS Synthetic.

```
XX WO200230986-A2.
XX 18-APR-2002.
XX 12-OCT-2001; 2001WO-US032140.
XX 13-OCT-2000; 2000US-0240285P.
XX 13-MAR-2001; 2001US-0275289P.
XX 21-JUN-2001; 2001US-0299987P.
XX (BIOI ) BIOGEN INC.
XX Garber E, Lyne P, Saldanha JW;
XX WPI; 2002-583337/62.
XX New humanized anti-lymphotoxin-beta receptor antibody, useful for
XX treating or reducing the advancement, severity or effects of neoplasia,
XX particularly solid tumors (i.e. carcinomas) including colorectal cancer
XX and breast cancer.
XX Example 5; Page 25-26; 41pp; English.
XX The present invention relates to humanised anti-lymphotoxin beta receptor
XX (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
XX binding antibody CBEL1 and can be used to treat neoplasia in humans. The
XX present sequence is a humanised murine CBEL1 heavy chain variable region
XX Sequence 449 AA;
XX
XX Query Match 72.9%; Score 2238.5; DB 5; Length 449;
XX Best Local Similarity 94.0%; Pred. No. 9.2e-110;
XX Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
XX
XX QY 1 EVQLVESGGDFVQPGGSLRVSQAAGSFAPSHYAMSWVRQAPGKGLEWYAYISSGSGTYY 60
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYIMYWFRAQPGKGLEWATISDGGSYTY 60
XX
XX QY 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 119
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 PDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 120
XX
XX QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 121 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
XX
XX QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 181 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 240
XX
XX QY 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 241 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300
XX
XX QY 300 STYRVSVLTVLHQDLWGKEYCKKVSNNKALPAPIETKISKAKGPQREPOVYTLPPSRDE 359
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 301 STYRVSVLTVLHQDLWGKEYCKKVSNNKALPAPIETKISKAKGPQREPOVYTLPPSRDE 360
XX
XX QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPDLSDGSGFFLYSKLTVDKSRW 419
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPDLSDGSGFFLYSKLTVDKSRW 420
XX
XX QY 420 QQGNVFCSCVMHEALHNNHYTKQSLSPG 448
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 421 QQGNVFCSCVMHEALHNNHYTKQSLSPG 449
XX
XX RESULT 14
XX ADQ07403
XX ID ADQ07403 standard; protein; 697 AA.
XX AC ADQ07403;
```

```
XX 07-OCT-2004 (first entry)
XX hCBEL1/hBHA10 bispecific-1 antibody construct mature heavy chain.
XX tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;
XX chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;
XX cancer; mature heavy chain; hCBEL1/hBHA10 bispecific-1.
XX Homo sapiens.
XX Synthetic.
XX WO2004058183-A2.
XX 15-JUL-2004.
XX 22-DEC-2003; 2003WO-US041243.
XX 20-DEC-2002; 2002US-0435185P.
XX (BIOG-) BIOGEN IDEC MA INC.
XX Lepage D, Gill A;
XX WPI; 2004-525785/50.
XX N-PSDB; ADQ07402.
XX Inhibiting tumor volume comprising administering an amount of a
XX lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic
XX agent (e.g. gemcitabine or adriamycin).
XX Disclosure; SEQ ID NO 2; 161pp; English.
XX The invention relates to a novel method for inhibiting tumour volume. The
XX method comprises administering an amount of a lymphotoxin-beta receptor
XX (LT-beta-R) agonist or antibody and an amount of at least one
XX chemotherapeutic agent, where the administration of the LT-beta-R agonist
XX or antibody and the chemotherapeutic agent results in supra-additive
XX inhibition of the tumour. The invention further relates to: a
XX pharmaceutical composition comprising an amount of an LT-beta-R agonist
XX and at least one chemotherapeutic agent, and a pharmaceutical carrier,
XX which upon administration to a subject results in supra-additive
XX inhibition of a tumour. The lymphotoxin-beta receptor agents have
XX cytostatic activity. Gene therapy may be used in the tumour inhibition
XX method. The method is useful for inhibiting tumour volume or for treating
XX cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic
XX agent are useful for preparing a medicament for the treatment of cancer,
XX which upon administration to a subject results in supra-additive
XX inhibition of a tumour. This sequence represents the mature heavy chain
XX of the hCBEL1/hBHA10 bispecific-1 antibody construct for use in the
XX tumour volume inhibition method of the invention.
XX Sequence 697 AA;
XX
XX Query Match 72.9%; Score 2238.5; DB 8; Length 697;
XX Best Local Similarity 94.0%; Pred. No. 1.4e-109;
XX Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
XX
XX QY 1 EVQLVESGGDFVQPGGSLRVSQAAGSFAPSHYAMSWVRQAPGKGLEWYAYISSGSGTYY 60
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYIMYWFRAQPGKGLEWATISDGGSYTY 60
XX
XX QY 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 119
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 PDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 120
XX
XX QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 121 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
XX
XX QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239
XX Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 181 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 240
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 44.1842 Seconds
(without alignments)
983.287 Million cell updates/sec

Title: US-10-089-500-53

perfect score: 3071

Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

POST-PROCESSING: Minimum Match 0%
Maximum Match 100%

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	2194.5	71.5	452	3	US-09-027-449-71	Sequence 71, Appl	
2	2194.5	71.5	452	3	US-09-026-985-71	Sequence 71, Appl	
3	2194.5	71.5	452	4	US-09-121-952A-71	Sequence 71, Appl	
4	2194.5	71.5	452	4	US-09-234-340A-71	Sequence 71, Appl	
5	2194.5	71.5	459	1	US-08-157-101A-7	Sequence 7, Appl	
6	2169	70.6	453	3	US-08-466-151-8	Sequence 8, Appl	
7	2169	70.6	453	3	US-08-462-163B-8	Sequence 8, Appl	
8	2169	70.6	453	4	US-09-802-096-8	Sequence 8, Appl	
9	2169	70.6	453	4	US-09-802-077-8	Sequence 8, Appl	
10	2167	70.6	451	2	US-08-887-352B-14	Sequence 14, Appl	
11	2167	70.6	451	2	US-08-887-352B-16	Sequence 16, Appl	
12	2167	70.6	451	3	US-08-466-151-65	Sequence 65, Appl	
13	2167	70.6	451	3	US-09-109-207C-14	Sequence 14, Appl	
14	2167	70.6	451	3	US-09-109-207C-16	Sequence 16, Appl	
15	2167	70.6	451	3	US-09-296-005-14	Sequence 14, Appl	
16	2167	70.6	451	3	US-09-296-005-16	Sequence 16, Appl	
17	2167	70.6	451	4	US-09-320-171-14	Sequence 14, Appl	
18	2167	70.6	451	4	US-09-320-171-16	Sequence 16, Appl	
19	2167	70.6	451	4	US-09-716-028-14	Sequence 14, Appl	
20	2167	70.6	451	4	US-09-716-028-16	Sequence 16, Appl	
21	2167	70.6	451	4	US-10-113-996-14	Sequence 14, Appl	
22	2167	70.6	451	4	US-10-113-996-16	Sequence 16, Appl	
23	2163	70.4	451	2	US-08-687-352B-18	Sequence 18, Appl	
24	2163	70.4	451	3	US-09-109-207C-18	Sequence 18, Appl	
25	2163	70.4	451	3	US-09-282-505-2	Sequence 2, Appl	
26	2163	70.4	451	3	US-09-054-255-2	Sequence 2, Appl	
27	2163	70.4	451	3	US-09-296-005-18	Sequence 18, Appl	

ALIGNMENTS

RESULT 1
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-027-449-71

Query Match 71.5%; Score 2194.5; DB 3; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.5e-161;
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFASFHYMSVWRQAPGKGLEWVAYISSGSGTYY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWRQAPGKGLEWVGYIDPSNGETTY 60
QY 61 SDSVKGRTTISRDNSTNTLYLQMSLRRAEDSAVYFCTRVKL---GTYYPDSWGQGLTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMSLRRAEDTAVYICARGDYRNGDWPFVWGQGLTLTV 120
QY 118 SSAATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVSVNSGALTSVGHHTPPAVLQ 177
DB 121 SSAATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVSVNSGALTSVGHHTPPAVLQ 180
QY 178 SSGLSLSVSVTPVSSSLGTQTYICNVNHPKNTKVDKVPKSCDKTHTCPCPAPELL 237
DB 181 SSGLSLSVSVTPVSSSLGTQTYICNVNHPKNTKVDKVPKSCDKTHTCPCPAPELL 240
QY 238 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQ 297

DB 241 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQ 300
QY 298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 357
DB 301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKS 417
DB 361 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKS 420
QY 418 RWQOGNVFSCSVMHALHNHYTQKSLSLSPGK 449
DB 421 RWQOGNVFSCSVMHALHNHYTQKSLSLSPGK 452
RESULT 2
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-71

Query Match 71.5%; Score 2194.5; DB 3; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.5e-161;
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFASFHYMSVWRQAPGKGLEWVAYISSGSGTYY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWRQAPGKGLEWVGYIDPSNGETTY 60
QY 61 SDSVKGRTTISRDNSTNTLYLQMSLRRAEDSAVYFCTRVKL---GTYYPDSWGQGLTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMSLRRAEDTAVYICARGDYRNGDWPFVWGQGLTLTV 120
QY 118 SSAATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVSVNSGALTSVGHHTPPAVLQ 177
DB 121 SSAATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVSVNSGALTSVGHHTPPAVLQ 180

Qy 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELL 237
Db 181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELL 240
Qy 238 GGPSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297
Db 241 GGPSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 300
Qy 298 YNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
Db 301 YNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 417
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 420
Qy 418 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 449
Db 421 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 452

RESULT 3

US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-71

Query Match 71.5%; Score 2194.5; DB 4; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.5e-161;

Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;
Qy 1 EVOLVESGGDFVQPGGSLRVSCAAGFAPFASHYAMVROAPGKGLWVAVISSGSGTYY 60
Db 1 EVOLVSGGGLVQPGGSLRVSCAAGFAPFASHYAMVROAPGKGLWVAVISSGSGTYY 60
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCRTVKL---GTYIFDSWGGTLLTV 117
Db 61 NQPKFKGRFTISRDNKNTLYLQMSLRADSAVYFCRTVKL---GTYIFDSWGGTLLTV 120
Qy 118 SSASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 177
Db 121 SSASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 180
Qy 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELL 237
Db 181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELL 240
Qy 238 GGPSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297
Db 241 GGPSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 300
Qy 298 YNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
Db 301 YNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 417
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 420
Qy 418 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 449
Db 421 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 452

RESULT 4
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998

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; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-234-340A-71

Query Match      71.5%; Score 2194.5; DB 4; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.5e-161;
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVS CAAGFAFASHYAMSVWRQAPGKLEWVAYISSGGSGTYY 60
DB 1 EVQLVQSGGGLVQPGGSLRLS CAAGSYSPFSHYMHWRQAPGKLEWVGIIDPSNGETTY 60
QY 61 SDSVKGRFTISRDN SKNTLYLQMRSLRAEDSAVYFCTRVKL---GTYVFDMSGQGLTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQWNSLRAEDTAVYICARGDYRYNGDWFVWGQGLTVTV 120
QY 118 SASTKGPSVFPPLAPS KSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 177
DB 121 SASTKGPSVFPPLAPS KSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 180
QY 178 SGLVSLSSVTVTPSS SLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPPCAPELL 237
DB 181 SGLVSLSSVTVTPSS SLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPPCAPELL 240
QY 238 GGPSVFLFPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 241 GGPSVFLFPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
QY 298 YNSTYRVSVLTVLHQD WLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
DB 301 YNSTYRVSVLTVLHQD WLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 417
DB 361 EMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
QY 418 RQQGNVFCSCVMHEALH NHYTKQSLSLSPGK 449
DB 421 RQQGNVFCSCVMHEALH NHYTKQSLSLSPGK 452

RESULT 5
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBc ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157.101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-157-101A-7

Query Match      71.5%; Score 2194.5; DB 1; Length 459;
Best Local Similarity 91.8%; Pred. No. 2.5e-161;
Matches 413; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVS CAAGFAFASHYAMSVWRQAPGKLEWVAYISSGGSGTYY 60
DB 10 QVQLVESGGVVPQGRSLRLS CAAGSFTFSSNSMHWVQAPGKLEWAVILYDGNHKFY 69
QY 61 SDSVKGRFTISRDN SKNTLYLQMRSLRAEDSAVYFCTRVK-LGTYVFDMSGQGLTLTVSS 119
DB 70 ADSVKGRFTISRDN SKNTLYLEVLSLQTEDTGYYCIRDQTYGVHFRFDSWGQGLTLTVSS 129
QY 120 ASTKGPSVFPPLAPS KSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 179
DB 130 ASTKGPSVFPPLAPS KSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 189
QY 180 GLYSLSVSVTVTPSS SLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPPCAPELLGG 239
DB 190 GLYSLSVSVTVTPSS SLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPPCAPELLGG 249
QY 240 PSVFLFPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
DB 250 PSVFLFPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 309
QY 300 STYRVSVLTVLHQD WLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 310 STYRVSVLTVLHQD WLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 369
QY 360 LTKNQVSLTCLVKG FYPSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 419
DB 370 LTKNQVSLTCLVKG FYPSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 429
QY 420 QQGNVFCSCVMHEALH NHYTKQSLSLSPGK 449
DB 430 QQGNVFCSCVMHEALH NHYTKQSLSLSPGK 459

RESULT 6
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
```

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genitech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/953-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-8

Query Match 70.6%; Score 2169; DB 3; Length 453;
Best Local Similarity 91.0%; Pred. No. 2.3e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAP--SHYAMSVVRQAPGKLEWVAYISSGSGTY 59
DB 1 EVOLVESGGGLVQPGGSLRVSCAASGFAP--SHYAMSVVRQAPGKLEWVAYISSGSGTY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYTFDSWGQGLTLTV 117
DB 60 YADSVKGRFTISRDDSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYTFDSWGQGLTLTV 119
QY 118 SSAST--KGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 175
DB 120 SSASTKKGKPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 179
QY 176 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVYTLPP 235
DB 180 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVYTLPP 239
QY 236 LLGGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 295
DB 240 LLGGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 299
QY 296 EQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPP 355
DB 300 EQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
DB 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

QY 416 KSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 449
DB 420 KSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 453
RESULT 7
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-08-466-163B-8

Query Match 70.6%; Score 2169; DB 3; Length 453;
Best Local Similarity 91.0%; Pred. No. 2.3e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAP--SHYAMSVVRQAPGKLEWVAYISSGSGTY 59
DB 1 EVOLVESGGGLVQPGGSLRVSCAASGFAP--SHYAMSVVRQAPGKLEWVAYISSGSGTY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYTFDSWGQGLTLTV 117
DB 60 YADSVKGRFTISRDDSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYTFDSWGQGLTLTV 119
QY 118 SSAST--KGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 175
DB 120 SSASTKKGKPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 179
QY 176 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVYTLPP 235
DB 180 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVYTLPP 239
QY 236 LLGGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 295
DB 240 LLGGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAV 299
QY 296 EQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPP 355
DB 300 EQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
DB 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419
QY 416 KSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 449
DB 420 KSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 453
RESULT 8
US-09-802-096-8
; Sequence 8, Application US/09802096

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; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P07182C2US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-096-8

Query Match 70.6%; Score 2169; DB 4; Length 453;
Best Local Similarity 91.0%; Pred. No. 2.3e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;

QY 1 EVOLVESGDFVQPGSLRVSCAASGPAF-SHYAMSWRQAPGKGLEWVAYISSGSGTY 59
Db 1 EVOLVESGGLVQPGSLRVSCAASGPAF-SHYAMSWRQAPGKGLEWVAYISSGSGTY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK--LGYTFDSMGQGLTVD 117
Db 60 YADSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK--LGYTFDSMGQGLTVD 117
QY 118 SSAST--KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 175
Db 118 SSAST--KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 175
QY 120 SSASTKKGKPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 179
Db 120 SSASTKKGKPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 179
QY 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 235
Db 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 235
QY 180 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 239
Db 180 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 239
QY 236 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
Db 236 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
QY 240 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 299
Db 240 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 299
QY 296 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
Db 296 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
QY 300 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
Db 300 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 415
Db 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 415
QY 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 419
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 419
QY 416 KSRWQOGNVFSCSVMHVHEALHNHYTQKSLSLSPGK 449
Db 416 KSRWQOGNVFSCSVMHVHEALHNHYTQKSLSLSPGK 453

RESULT 9
US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. 669472
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P07182C2US
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; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

Query Match 70.6%; Score 2169; DB 4; Length 453;
Best Local Similarity 91.0%; Pred. No. 2.3e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;

QY 1 EVOLVESGDFVQPGSLRVSCAASGPAF-SHYAMSWRQAPGKGLEWVAYISSGSGTY 59
Db 1 EVOLVESGGLVQPGSLRVSCAASGPAF-SHYAMSWRQAPGKGLEWVAYISSGSGTY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK--LGYTFDSMGQGLTVD 117
Db 60 YADSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK--LGYTFDSMGQGLTVD 117
QY 118 SSAST--KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 175
Db 118 SSAST--KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 175
QY 120 SSASTKKGKPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 179
Db 120 SSASTKKGKPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAV 179
QY 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 235
Db 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 235
QY 180 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 239
Db 180 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPPCPAPE 239
QY 236 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
Db 236 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
QY 240 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 299
Db 240 LLGSPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 299
QY 296 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
Db 296 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
QY 300 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
Db 300 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 415
Db 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 415
QY 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 419
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 419
QY 416 KSRWQOGNVFSCSVMHVHEALHNHYTQKSLSLSPGK 449
Db 416 KSRWQOGNVFSCSVMHVHEALHNHYTQKSLSLSPGK 453

RESULT 10
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```

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; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-14

Query Match 70.6%; Score 2167; DB 2; Length 451;
Best Local Similarity 90.9%; Pred. No. 3.3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVQLVESGGGVQPGGSLRVSCTASGFAF-SHYAMSVVRQAPGKLEWVAYISSGGSGTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASITVDGS-TN 59
QY 60 YSDSVKGRFTISRDNSKNTLYLQMSRLRAEDSAVYFCFTRVK--LGTYYPDSWGQGLT 117
Db 60 YNPVKGRITISRDDSKNTFLQMSRLRAEDTAVYYCARGSHYFGHHFAVWGQGLT 119
QY 118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 177
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 179
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 237
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 239
QY 238 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 297
Db 240 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299
QY 298 YNSTYRVSVSLTVLHODWLNKGYCKKSVNKPALPAIEKTSKAKGQPREPQVYTLPPSR 357
Db 300 YNSTYRVSVSLTVLHODWLNKGYCKKSVNKPALPAIEKTSKAKGQPREPQVYTLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 417
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 419
QY 418 RWOQGNVFCVSNMHEALHNHYTQKSLSLSPGK 449
Db 420 RWOQGNVFCVSNMHEALHNHYTQKSLSLSPGK 451

RESULT 11
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

```

```

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-16

Query Match 70.6%; Score 2167; DB 2; Length 451;
Best Local Similarity 90.9%; Pred. No. 3.3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVQLVESGGGVQPGGSLRVSCTASGFAF-SHYAMSVVRQAPGKLEWVAYISSGGSGTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASITVDGS-TN 59
QY 60 YSDSVKGRFTISRDNSKNTLYLQMSRLRAEDSAVYFCFTRVK--LGTYYPDSWGQGLT 117
Db 60 YNPVKGRITISRDDSKNTFLQMSRLRAEDTAVYYCARGSHYFGHHFAVWGQGLT 119
QY 118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 177
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 179
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 237
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 239
QY 238 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 297
Db 240 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299
QY 298 YNSTYRVSVSLTVLHODWLNKGYCKKSVNKPALPAIEKTSKAKGQPREPQVYTLPPSR 357
Db 300 YNSTYRVSVSLTVLHODWLNKGYCKKSVNKPALPAIEKTSKAKGQPREPQVYTLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 417
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 419
QY 418 RWOQGNVFCVSNMHEALHNHYTQKSLSLSPGK 449
Db 420 RWOQGNVFCVSNMHEALHNHYTQKSLSLSPGK 451

RESULT 12
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3.3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;
QY 1 EVQLVESGGDFVQPGGSLRVS CAASGFAP- SHYAMSVWROAPGKGLEWVAYISSGGSGTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNWIROAPGKGLEWVASYIDGS-TN 59
QY 60 YSDSVKGRFTISRDN SKNTLYLQMRSLRAEDSAVYFCFTRVK--LGTYYPDSWGQGTLTIV 117
DB 60 YNPYSVKGRITISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHHWFAVWGQGLTVTV 119
QY 118 SSASTKGPSVFPFLAPSSKTS GGTAAALGCLVKDYKPEPTVTVSNWNSGALTSVHTTTPAVLQ 177
DB 118 SSASTKGPSVFPFLAPSSKTS GGTAAALGCLVKDYKPEPTVTVSNWNSGALTSVHTTTPAVLQ 179
QY 178 SSGLYSLSSVTVTPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELL 237
DB 180 SSGLYSLSSVTVTPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELL 239
QY 238 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
QY 298 YNSTRVVSVLTIVLHODWLN GKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 357
DB 300 YNSTRVVSVLTIVLHODWLN GKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 417
DB 360 EEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 419
QY 418 RWQGNVFSCSVMHEALHNHYTQK SLSLSPGK 449
DB 420 RWQGNVFSCSVMHEALHNHYTQK SLSLSPGK 451

Db 360 EEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 419
QY 418 RWQGNVFSCSVMHEALHNHYTQK SLSLSPGK 449
Db 420 RWQGNVFSCSVMHEALHNHYTQK SLSLSPGK 451
RESULT 13
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3.3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;
QY 1 EVQLVESGGDFVQPGGSLRVS CAASGFAP- SHYAMSVWROAPGKGLEWVAYISSGGSGTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNWIROAPGKGLEWVASYIDGS-TN 59
QY 60 YSDSVKGRFTISRDN SKNTLYLQMRSLRAEDSAVYFCFTRVK--LGTYYPDSWGQGTLTIV 117
DB 60 YNPYSVKGRITISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHHWFAVWGQGLTVTV 119
QY 118 SSASTKGPSVFPFLAPSSKTS GGTAAALGCLVKDYKPEPTVTVSNWNSGALTSVHTTTPAVLQ 177
DB 118 SSASTKGPSVFPFLAPSSKTS GGTAAALGCLVKDYKPEPTVTVSNWNSGALTSVHTTTPAVLQ 179
QY 178 SSGLYSLSSVTVTPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELL 237
DB 180 SSGLYSLSSVTVTPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELL 239
QY 238 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
QY 298 YNSTRVVSVLTIVLHODWLN GKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 357
DB 300 YNSTRVVSVLTIVLHODWLN GKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 417
DB 360 EEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 419
QY 418 RWQGNVFSCSVMHEALHNHYTQK SLSLSPGK 449
DB 420 RWQGNVFSCSVMHEALHNHYTQK SLSLSPGK 451

RESULT 14
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3.3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

Qy 1 EVOLVESGGDFVOPGGSLRVSCAASGAPF-SHYAMSVVROAPGKGLEWVAYISGGSGTY 59
Db 1 EVOLVESGGGLVOPGGSLRLSCAVSGYSITSGYSWNIROAPGKGLEWVASITYDGS-TN 59
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCFTRVK--LGTYYFDSWQOGLTLTV 117
Db 60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHHFAVWQOGLTLTV 119
Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 177
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 179
Qy 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 237
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 239
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
Db 240 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 298 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSR 357
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSR 359
Qy 358 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 417
Db 360 EEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 419
Qy 418 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 449
Db 420 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 451

RESULT 15
US-09-296-005-14
Sequence 14. Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:

NAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3.3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

Qy 1 EVOLVESGGDFVOPGGSLRVSCAASGAPF-SHYAMSVVROAPGKGLEWVAYISGGSGTY 59
Db 1 EVOLVESGGGLVOPGGSLRLSCAVSGYSITSGYSWNIROAPGKGLEWVASITYDGS-TN 59
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCFTRVK--LGTYYFDSWQOGLTLTV 117
Db 60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHHFAVWQOGLTLTV 119
Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 177
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 179
Qy 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 237
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 239
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
Db 240 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 298 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSR 357
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSR 359
Qy 358 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 417
Db 360 EEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 419
Qy 418 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 449
Db 420 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 451

Search completed: August 1, 2005, 09:20:52
Job time : 46.1842 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 153.558 Seconds
(without alignments)
1476.651 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVQLVESGGDFVQPGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2750.5	89.6	579	14	US-10-138-727A-41
2	2750.5	89.6	579	14	US-10-310-719-32
3	2719.5	88.6	575	16	US-10-737-208A-6
4	2621	85.3	580	14	US-10-310-719-37
5	2589	84.3	580	14	US-10-310-719-35
6	2246.5	73.2	447	15	US-10-474-832-4
7	2240.5	73.0	447	15	US-10-474-832-5
8	2238.5	72.9	4852	15	US-10-412-406-32
9	2238.5	72.9	4852	15	US-10-412-406-33
10	2236.5	72.8	447	15	US-10-474-832-6
11	2236	72.8	464	17	US-10-938-353-102
					Sequence 41, Appl
					Sequence 32, Appl
					Sequence 37, Appl
					Sequence 35, Appl
					Sequence 4, Appl
					Sequence 5, Appl
					Sequence 32, Appl
					Sequence 33, Appl
					Sequence 6, Appl
					Sequence 102, Appl

445	14	US-10-320-231A-79	Sequence 79, Appl
445	17	US-10-867-506-79	Sequence 79, Appl
449	17	US-10-476-265-12	Sequence 12, Appl
468	17	US-10-476-265-20	Sequence 20, Appl
444	14	US-10-150-475A-6	Sequence 6, Appl
444	16	US-10-704-522-6	Sequence 6, Appl
444	16	US-10-645-215-6	Sequence 98, Appl
470	17	US-10-938-353-98	Sequence 98, Appl
449	9	US-09-736-371B-21	Sequence 21, Appl
449	15	US-10-463-442-21	Sequence 21, Appl
477	15	US-10-291-265-385	Sequence 385, Appl
446	15	US-10-408-901-38	Sequence 3, Appl
474	10	US-09-848-832-3	Sequence 3, Appl
474	14	US-10-225-108A-3	Sequence 1, Appl
474	15	US-10-461-148-1	Sequence 1, Appl
442	15	US-10-226-435A-12	Sequence 12, Appl
442	16	US-10-487-326-12	Sequence 12, Appl
442	16	US-10-486-908-12	Sequence 12, Appl
442	18	US-10-513-527-12	Sequence 12, Appl
451	9	US-09-822-698A-26	Sequence 26, Appl
449	17	US-10-985-584-10	Sequence 10, Appl
445	15	US-10-408-901-34	Sequence 34, Appl
442	16	US-10-487-322-12	Sequence 12, Appl
442	16	US-10-487-326-21	Sequence 21, Appl
442	16	US-10-486-908-16	Sequence 16, Appl
442	18	US-10-513-527-21	Sequence 21, Appl
453	17	US-10-891-658-41	Sequence 41, Appl
446	15	US-10-408-901-46	Sequence 46, Appl
469	16	US-10-858-186-14	Sequence 14, Appl
469	15	US-10-656-769-26	Sequence 26, Appl
445	15	US-10-408-901-42	Sequence 42, Appl
452	15	US-09-726-258-71	Sequence 71, Appl
452	17	US-10-861-049-46	Sequence 46, Appl
469	15	US-10-656-769-20	Sequence 20, Appl
474	15	US-10-108-260A-4640	Sequence 4640, Appl
713	16	US-10-679-620-64	Sequence 64, Appl
715	16	US-10-679-620-62	Sequence 62, Appl
448	17	US-10-985-584-18	Sequence 18, Appl
452	16	US-10-818-765-4	Sequence 4, Appl
452	17	US-10-861-049-16	Sequence 16, Appl
471	17	US-10-877-363-4	Sequence 4, Appl
471	17	US-10-922-651-4	Sequence 4, Appl
471	17	US-10-861-049-4	Sequence 4, Appl
446	15	US-10-408-901-30	Sequence 30, Appl
446	15	US-10-408-901-50	Sequence 50, Appl
447	16	US-10-379-392-116	Sequence 116, Appl
447	16	US-10-379-392-117	Sequence 117, Appl
452	17	US-10-861-049-20	Sequence 20, Appl
451	15	US-10-423-299-4	Sequence 4, Appl
447	16	US-10-379-392-141	Sequence 141, Appl
447	16	US-10-423-299-4	Sequence 4, Appl
452	17	US-10-861-049-17	Sequence 17, Appl
452	17	US-10-861-049-11	Sequence 11, Appl
471	17	US-10-861-049-11	Sequence 11, Appl
464	15	US-10-032-037B-26	Sequence 26, Appl
464	15	US-10-029-988B-26	Sequence 26, Appl
464	15	US-10-032-423A-26	Sequence 26, Appl
464	15	US-10-029-926B-26	Sequence 26, Appl
472	15	US-10-108-260A-4073	Sequence 4073, Appl
449	16	US-10-635-908-16	Sequence 16, Appl
449	16	US-10-635-908-18	Sequence 18, Appl
453	9	US-09-802-077-8	Sequence 8, Appl
453	9	US-09-802-096-8	Sequence 8, Appl
453	10	US-09-925-179-8	Sequence 8, Appl
453	17	US-10-968-237-8	Sequence 14, Appl
451	9	US-09-920-171-14	Sequence 16, Appl
451	9	US-09-920-171-16	Sequence 65, Appl
451	14	US-10-113-996-14	Sequence 14, Appl
451	14	US-10-113-986-14	Sequence 16, Appl
451	16	US-10-813-483-16	Sequence 4, Appl
451	16	US-10-813-483-5	Sequence 5, Appl
451	16	US-10-791-619-14	Sequence 14, Appl

85 2167 70.6 451 16 US-10-791-619-16 Sequence 16, Appl
86 2167 70.6 451 17 US-10-714-000-2 Sequence 2, Appl
87 2167 70.6 451 17 US-10-698-073-9 Sequence 9, Appl
88 2167 70.6 451 17 US-10-968-237-65 Sequence 65, Appl
89 2167 70.6 451 20 US-11-013-966-4 Sequence 4, Appl
90 2167 70.6 451 20 US-11-013-966-5 Sequence 5, Appl
91 2167 70.6 476 14 US-10-020-786-11 Sequence 11, Appl
92 2167 70.6 476 17 US-10-697-995-9 Sequence 9, Appl
93 2167 70.6 667 16 US-10-764-428-7 Sequence 7, Appl
94 2167 70.6 669 16 US-10-764-428-21 Sequence 21, Appl
95 2166.5 70.5 447 16 US-10-379-392-143 Sequence 143, App
96 2165 70.5 451 17 US-10-698-073-7 Sequence 7, Appl
97 2164 70.5 451 10 US-09-925-179-66 Sequence 66, Appl
98 2164 70.5 451 17 US-10-968-237-66 Sequence 66, Appl
99 2163 70.4 451 9 US-09-920-171-18 Sequence 18, Appl
100 2163 70.4 451 10 US-09-792-938-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-138-727A-41
; Sequence 41, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Susan
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/10/138,727A
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain-IL2
US-10-138-727A-41

Query Match 89.6%; Score 2750.5; DB 14; Length 579;
Best Local Similarity 88.5%; Pred. No. 6.4e-166;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

QY 1 EVLVESGDDFVQPGSLRVSCAASGFAFASHYAMSWVRQAPGKGLWVAYISSGSGGTYY 60
DB 1 QIQLVQSGAEVKKPQETVKISKASGYFTTNYGMNWKQTGPKGLKMWGWINTYTGPTY 60
61 SDSVKGRTTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYVYFDSWGGTLLTVSS 119
DB 61 ADDFKGRFTTIAETSTSTLYLQNLNRSEDATATYFCVRFISKGDY----WGQGTIVTVSS 116
120 ASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
DB 61 ADDFKGRFAFSLTSTAFQINNLNRSEDATATYFCVRFISKGDY----WGQGTIVTVSS 116
177 GLYSLSVVTVVPSVSSSLGTQTYICNVNHPKPSNTKVDKRVPEKSCDKTHTCPCPAPPELLGG 236
QY 180 GLYSLSVVTVVPSVSSSLGTQTYICNVNHPKPSNTKVDKRVPEKSCDKTHTCPCPAPPELLGG 239
DB 177 GLYSLSVVTVVPSVSSSLGTQTYICNVNHPKPSNTKVDKRVPEKSCDKTHTCPCPAPPELLGG 236
240 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNNAKTPREEQYN 299
DB 237 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNNAKTPREEQYN 296
300 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 359
QY 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 356
360 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
DB 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 356

QY 360 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
DB 357 MTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 416
420 QQGNVFSVSMHEALHNHYTQKSLSLSPGKAPTSSTSTKKTQLQLEHLLLDLQMLNGINN 479
DB 417 QQGNVFSVSMHEALHNHYTQKSLSLSPGKAPTSSTSTKKTQLQLEHLLLDLQMLNGINN 476
480 YKNPKLTMLTFTKFPMPKKATLKHLCLEBELKPLEEVLNLAQSKNPHLRPRDLISIN 539
DB 477 YKNPKLTMLTFTKFPMPKKATLKHLCLEBELKPLEEVLNLAQSKNPHLRPRDLISIN 536
540 VIVLELKGSETFMCCEYADETATIVFELNRWITFCQSIISTLT 582
DB 537 VIVLELKGSETFMCCEYADETATIVFELNRWITFCQSIISTLT 579

RESULT 2
US-10-310-719-32
; Sequence 32, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant
US-10-310-719-32

Query Match 89.6%; Score 2750.5; DB 14; Length 579;
Best Local Similarity 88.5%; Pred. No. 6.4e-166;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

QY 1 EVLVESGDDFVQPGSLRVSCAASGFAFASHYAMSWVRQAPGKGLWVAYISSGSGGTYY 60
DB 1 QIQLVQSGPELKKPGSSVKISKASGYFTTNYGMNWKQTGPKGLKMWGWINTYTGPTY 60
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DB 117 ASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 176
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360 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
DB 357 MTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 416

Qy 420 QQGVFSCVWHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINN 479
Db 417 QQGVFSCVWHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINN 476
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHQCLBEELKPLEEVNLQAQSKNFHLRPRDLISNIN 539
Db 477 YKNPKLTRMLTFKPYMPKKATELKHQCLBEELKPLEEVNLQAQSKNFHLRPRDLISNIN 536
Qy 540 VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 582
Db 537 VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 579
RESULT 3
US-10-737-208A-6
; Sequence 6, Application US/10737208A
; Publication No. US20040203100A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
; FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2
US-10-737-208A-6
Query Match 88.6%; Score 2719.5; DB 16; Length 575;
Best Local Similarity 89.0%; Pred. No. 5.8e-164;
Matches 518; Conservative 24; Mismatches 33; Indels 7; Gaps 3;
Qy 1 EVOLVSGDGFVQPGGSLRVSCAASGFAFASHYAMSWRQAPGKLEWVAYISSGGSGTY 60
Db 1 EVOLVSGAVERPGASVKLSCKASGSSFTGYNNWVRQINQISLEWIGDAIDPYGQTSY 60
Qy 61 SDVSKGRFTISRDNKNTLYQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSSA 120
Db 61 NQKFKGRATLTVDKSTASTAMHLKSLSEDTAYVCVS---GNEY---WGQGTSTVTVSSA 114
Qy 121 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180
Db 115 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 174
Qy 181 LYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPPCPAPELLGGP 240
Db 175 LYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPPCPAPELLGGP 234
Qy 241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYNS 300
Db 235 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYNS 294
Qy 301 TYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDEL 360
Db 295 TYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDEM 354
Qy 361 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQ 420
Db 355 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQ 414
Qy 421 QGNVFCVSMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINN 480
Db 415 QGNVFCVSMHEALHNHYTQKSLSLSPG-APTSSSTKKTQLQLEHLLDLQMLNGINN 473
Qy 481 KNPKLTRMLTFKPYMPKKATELKHQCLBEELKPLEEVNLQAQSKNFHLRPRDLISNIN 540

Db 474 KNPKLTRMLTFKPYMPKKATELKHQCLBEELKPLEEVNLQAQSKNFHLRPRDLISNIN 533
Qy 541 IVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 582
Db 534 IVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 575
RESULT 4
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dI-NHS76 (gamma4h) (FN=AAQ)-aIa-IL2 (D20T) heavy chain fused to
US-10-310-719-37
Query Match 85.1%; Score 2621; DB 14; Length 580;
Best Local Similarity 85.8%; Pred. No. 1e-157;
Matches 500; Conservative 29; Mismatches 50; Indels 4; Gaps 3;
Qy 1 EVOLVSGDGFVQPGGSLRVSCAASGFAFASH-YAMSWRQAPGKLEWVAYISSGGSGTY 59
Db 1 QVQLVSSGFLGVKPKSETLSITCAVSCYSISSGYWGMIRQPPCKGLEWIGSIYHSGS-TY 59
Qy 60 YSDVSKGRFTISRDNKNTLYQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
Db 60 YNPGLSKRVITISVDTSKQPSLKLSSVTAADTAAYYCARGKWSK--FDYWGQGTLLTVSS 117
Qy 120 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179
Db 118 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 177
Qy 180 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPPCPAPELLGG 239
Db 178 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPPCPAPELLGG 237
Qy 240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQY 299
Db 238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQY 297
Qy 300 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 359
Db 298 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 357
Qy 360 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 419
Db 358 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 417
Qy 420 QGNVFCVSMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINN 479
Db 418 QGNVFCVSMHEALHNHYTQKSLSLSPGAPTSSSTKKTQLQLEHLLDLQMLNGINN 477
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHQCLBEELKPLEEVNLQAQSKNFHLRPRDLISNIN 539
Db 478 YKNPKLTRMLTFKPYMPKKATELKHQCLBEELKPLEEVNLQAQSKNFHLRPRDLISNIN 537

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QY 540 VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISLT 582
Db 538 VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISLT 580

RESULT 5
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: dI-NHS76 (gamma2h) (FN>A>) -ala-IL2 (D20T) heavy chain fused to IL2
; OTHER INFORMATION: variant
US-10-310-719-35

Query Match 84.3%; Score 2589; DB 14; Length 580;
Best Local Similarity 85.1%; Pred. No. 1.1e-155;
Matches 497; Conservative 29; Mismatches 52; Indels 6; Gaps 5;

QY 1 EVOLVESGDFVQPGSLRVSCAASGFAPSH-YAMSWVRQAPGKLEWVAISSGGSGTY 59
Db 1 QVOLQESGFLVKPSETSLTCAVSGYSISSGYWGWIRQPPGKLEWIGSIYHSGS-TY 59

QY 60 YSDSVKGRFTIRSDNSKNTLYLQMSLRADSAVFCFTRVKLGTYYFPDSWQGTLLTVSS 119
Db 60 YNPSLSKRVTSIVDTISKQFSLKSLSVTAADTAVYYCARGKWSK--FDYMQQGTLLTVSS 117

QY 120 -ASTKGPSVFPLAPSSKSTSGGTAAALGLCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQS 178
Db 118 GASTKGPSVFPLAPCSRSTSESTAAALGLCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQS 177

QY 179 SGLYSLSVVTVVPSSSLGNTQYICNNHKKPSNTKVDKVEPKSCDKTHTCPCPAPELLG 238
Db 178 SGLYSLSVVTVVPSSSNFGQTTCNVDHKKPSNTKVDKVEPKSCDKTHTCPCPAPP-VA 236

QY 239 GPSVFLLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPREEQY 298
Db 237 GPSVFLLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNWYVDGVEVHNAAKTPREEQA 296

QY 299 NSTYRVVSVLTVHLQDWLNGKEYCKVSKNALPAPIEKTISKAKQPREPQVYITLPSRD 358
Db 297 QSTFRVSVSVTVHVDWMLNGKEYCKVSKNGLPAPIEKTISKTKQPREPQVYITLPPSRE 356

QY 359 ELTKNOVSLTCLVKGPYPSPDIAVESNGQPNNTKTPPVLDSDGSPFLYSKLTVDKSR 418
Db 357 EMTKNOVSLTCLVKGPYPSPDIAVESNGQPNNTKTPPVLDSDGSPFLYSKLTVDKSR 416

QY 419 WOQGNVFCSCVMHEALHNNHYTKQSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGIN 478
Db 417 WOQGNVFCSCVMHEALHNNHYTKSATATPGAAPTSSSTKTKTQLQLEHLLLDLQMLINGIN 476

QY 479 NYKNPKLTQMLTKFVMPKATKELKHLQCLLEELKPLEVLNLAQSKNPHLRPDLISNI 538
Db 477 NYKNPKLTQMLTKFVMPKATKELKHLQCLLEELKPLEVLNLAQSKNPHLRPDLISNI 536

QY 539 NVIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISLT 582
Db 537 NVIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISLT 580

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; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-5

Query Match          73.08; Score 2240.5; DB 15; Length 447;
Best Local Similarity 94.9%; Pred. No. 9.5e-134;
Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVLVESGGDFVOPGGSLRVSCAASGFAPFASHYAMSWVRQAPGKGLEWVAIVISSGSGTTY 60
   |||||
Db 1 EVLVESGGGLVOPGGSLRVSCAASGFTFSRYTMSWVRQAPGKGLEWVAIVISSGHH-TYY 59
   |||||

QY 61 SDVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGLTLTVSSA 120
   |||||
Db 60 LDSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYCTRGFGDGYFDVWGQGLTLTVSSA 119
   |||||

QY 121 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180
   |||||
Db 120 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 179
   |||||

QY 181 LYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTCCPCPAPELLGGP 240
   |||||
Db 180 LYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTCCPCPAPELLGGP 239
   |||||

QY 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
   |||||
Db 240 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQS 299
   |||||

QY 301 TYRWSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRDEL 360
   |||||
Db 300 TYRWSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRDEL 359
   |||||

QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420
   |||||
Db 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 419
   |||||

QY 421 QGNVFSCVMHEALHNHYTQKSLSLSPG 448
   |||||
Db 420 QGNVFSCVMHEALHNHYTQKSLSLSPG 447
   |||||
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RESULT 8
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINALOOCN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
```

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; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-412-406-32

Query Match          72.9%; Score 2238.5; DB 15; Length 663;
Best Local Similarity 94.0%; Pred. No. 2e-133;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVLVESGGDFVOPGGSLRVSCAASGFAPFASHYAMSWVRQAPGKGLEWVAIVISSGSGTTY 60
   |||||
Db 215 EVLVESGGGLVKPGGSLRVSCAASGFTFSYYWYFRQAPGKGLEWVAIVISSGSGTTY 274
   |||||

QY 61 SDVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGLTLTVSS 119
   |||||
Db 275 POSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYCARBENGNYFYFDYWGQGLTLTVSS 334
   |||||

QY 120 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179
   |||||
Db 335 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 394
   |||||

QY 180 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTCCPCPAPELLGG 239
   |||||
Db 395 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTCCPCPAPELLGG 454
   |||||

QY 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
   |||||
Db 455 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 514
   |||||

QY 300 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRDE 359
   |||||
Db 515 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRDE 574
   |||||

QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 419
   |||||
Db 575 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 634
   |||||

QY 420 QGNVFSCVMHEALHNHYTQKSLSLSPG 448
   |||||
Db 635 QGNVFSCVMHEALHNHYTQKSLSLSPG 663
   |||||
```

```
RESULT 9
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINALOOCN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4852
; TYPE: PRT
; ORGANISM: Homo Sapien
```

US-10-412-406-33

Query Match 72.9%; Score 2238.5; DB 15; Length 4852;
Best Local Similarity 94.0%; Pred. No. 2.1e-132;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
QY 1 EVQLVESGGDFVQPGGSLRVSCAAGFPAPSHYAMSWRQAPGKLEWVAIYSSGGSTYY 60
DB 4404 EVQLVESGGGLVQPGGSLRVSCAAGFTFSDYIMTFWFRQAPGKLEWVAIYSSGGSTYY 4463
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDWSWGQGLTLTVSS 119
DB 4464 PDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDWSWGQGLTLTVSS 4523
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSS 179
DB 4524 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSS 4583
QY 180 GLYSLSVVTVPSSSISLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGG 239
DB 4584 GLYSLSVVTVPSSSISLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGG 4643
QY 240 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
DB 4644 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 4703
QY 300 STYRVSVLTVLHQQDLWNGKEYCKVSKNALKAPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 4704 STYRVSVLTVLHQQDLWNGKEYCKVSKNALKAPAPIEKTISKAKGQPREPQVYTLPPSRDE 4763
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 419
DB 4764 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 4823
QY 420 QGNVFSCSVMEALHNHYTQKSLSLSPG 448
DB 4824 QGNVFSCSVMEALHNHYTQKSLSLSPG 4852

RESULT 10

US-10-474-832-6
; Sequence 6, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
US-10-474-832-6

Query Match 72.8%; Score 2236.5; DB 15; Length 447;
Best Local Similarity 94.6%; Pred. No. 1.7e-133;
Matches 424; Conservative 4; Mismatches 19; Indels 1; Gaps 1;
QY 1 EVQLVESGGDFVQPGGSLRVSCAAGFPAPSHYAMSWRQAPGKLEWVAIYSSGGSTYY 60
DB 1 EVQLVESGGGLVQPGGSLRVSCAAGFTFSDYIMTFWFRQAPGKLEWVAIYSSGGSTYY 59
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDWSWGQGLTLTVSS 120

DB 60 LDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDWSWGQGLTLTVSS 119
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSSG 180
DB 120 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSSG 179
QY 181 LYSLSVVTVPSSSISLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 240
DB 180 LYSLSVVTVPSSSISLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 239
QY 241 SVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
DB 240 SVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299
QY 301 TYRVSVLTVLHQQDLWNGKEYCKVSKNALKAPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
DB 300 TYRVSVLTVLHQQDLWNGKEYCKVSKNALKAPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQ 420
DB 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQ 419
QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPG 448
DB 420 QGNVFSCSVMEALHNHYTQKSLSLSPG 447

RESULT 11

US-10-938-353-102
; Sequence 102, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 102
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-102

Query Match 72.8%; Score 2236; DB 17; Length 464;
Best Local Similarity 93.5%; Pred. No. 1.9e-133;
Matches 420; Conservative 11; Mismatches 14; Indels 4; Gaps 1;
QY 1 EVQLVESGGDFVQPGGSLRVSCAAGFPAPSHYAMSWRQAPGKLEWVAIYSSGGSTYY 60
DB 20 QVQLVESGGGLVQPGGSLRVSCAAGFTFSDYIMSWIRQAPGKLEWVAIYSSGGSTYY 79
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDWSWGQGLTLTVSS 120
DB 80 ADSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDWSWGQGLTLTVSS 135
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSSG 180
DB 136 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSSG 195
QY 181 LYSLSVVTVPSSSISLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 240
DB 196 LYSLSVVTVPSSSISLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 255

QY 241 SVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
DB 256 SVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 315
QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 360
DB 316 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 375
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 420
DB 376 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 435
QY 421 QGNVFSCVMHEALHNHYTQKSLSLSPGK 449
DB 436 QGNVFSCVMHEALHNHYTQKSLSLSPGK 464

RESULT 12
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79

Query Match 72.8%; Score 2234.5; DB 14; Length 445;
Best Local Similarity 94.4%; Pred. No. 2.3e-133;
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
QY 4 LVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVROAPGKLEWVAYISGGSGTYSDS 63
DB 1 LVESGGGLVQPGSLRLSCLSAASGFTFSSYAMSWVROAPGKLEWVSAISGGSGTYADS 60
QY 64 VKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSNGQGTLLTVSSASTK 123
DB 61 VKGRFTISRDNKNTLYLQMRSLRAEDTAVYICARRDFFA-HFDVWGQGTLLTVSSASTK 119
QY 124 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 183
DB 120 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 179
QY 184 LSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 243
DB 180 LSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 239
QY 244 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 303
DB 180 LSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 239
QY 244 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 303
DB 240 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299
QY 304 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 363
DB 240 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299
QY 304 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 363
DB 300 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 359
QY 364 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 423
DB 300 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 359
QY 364 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 423
DB 300 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 359

DB 360 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 419
QY 424 VFLSCVMHEALHNHYTQKSLSLSPGK 449
DB 420 VFLSCVMHEALHNHYTQKSLSLSPGK 445

RESULT 13
US-10-867-506-79
; Sequence 79, Application US/10867506
; Publication No. US20050112698A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; APPLICANT: Delaria, Kathy
; APPLICANT: Yan, Kelly
; APPLICANT: Wong, Teresa
; APPLICANT: Longphre, Malinda
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 11334*10
; CURRENT APPLICATION NUMBER: US/10/867,506
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 10/320,231
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-867-506-79

Query Match 72.8%; Score 2234.5; DB 17; Length 445;
Best Local Similarity 94.4%; Pred. No. 2.3e-133;
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
QY 4 LVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVROAPGKLEWVAYISGGSGTYSDS 63
DB 1 LVESGGGLVQPGSLRLSCLSAASGFTFSSYAMSWVROAPGKLEWVSAISGGSGTYADS 60
QY 64 VKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSNGQGTLLTVSSASTK 123
DB 61 VKGRFTISRDNKNTLYLQMRSLRAEDTAVYICARRDFFA-HFDVWGQGTLLTVSSASTK 119
QY 124 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 183
DB 120 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 179
QY 184 LSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 243
DB 180 LSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 239
QY 244 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 303
DB 240 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299
QY 304 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 363
DB 300 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 359
QY 364 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 423
DB 360 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 419
QY 424 VFLSCVMHEALHNHYTQKSLSLSPGK 449
DB 420 VFLSCVMHEALHNHYTQKSLSLSPGK 445

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 32.9571 Seconds
(without alignments)
1699.125 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVLVESGGDFVQPGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	57.5	330	1 GHU	Ig gamma-1 chain C
2	1630.5	53.1	377	2 A23511	Ig gamma-3 chain C
3	1628.5	53.0	377	2 A60764	Ig gamma-3 chain C
4	1604	52.2	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	51.8	327	1 G4HU	Ig gamma-4 chain C
6	1508.5	49.1	444	2 PC4436	monoclonal antibod
7	1487	48.4	470	2 S22080	Ig heavy chain pre
8	1440.5	46.9	469	2 S37483	Ig gamma-2a chain
9	1437	46.8	446	2 S40295	Ig gamma-2a chain
10	1434	46.7	472	2 S31459	Ig gamma-1 chain -
11	1429	46.5	374	2 S69339	Ig heavy chain V r
12	1390	45.3	474	1 G2MS11	Ig gamma-2b chain
13	1367.5	44.5	475	2 S01321	Ig gamma-2b chain
14	1263	41.1	328	2 I47159	Ig gamma 2a chain
15	1260	41.0	255	4 S31866	Ig gamma-1 chain C
16	1257	40.9	328	2 I47160	Ig gamma 2b chain
17	1254	40.8	234	2 PT0207	Ig gamma chain C r
18	1231	40.1	328	2 I47158	Ig gamma 1 chain C
19	1230.5	40.1	323	1 GHRB	Ig gamma chain C r
20	1227	40.0	328	2 I47161	Ig gamma 3 chain C
21	1216.5	39.6	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2 C30554	Ig heavy chain C r
23	1152	37.5	326	2 PS0017	Ig gamma-1 chain C
24	1151	37.5	289	1 G3HUM1	Ig gamma-3 heavy c
25	1146.5	37.3	333	2 PS0018	Ig gamma-2b chain
26	1142	37.2	324	1 G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1 G1MSC	Ig gamma-3 chain C
28	1139	37.1	393	1 G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1 G3MSM	Ig gamma-3 chain C

30	1126	36.7	330	1 G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1 G2MSAB	Ig gamma-2a chain
32	1121	36.5	339	1 G2MSAM	Ig gamma-2a chain
33	1118.5	36.4	329	2 S00847	Ig gamma-2c chain
34	1112	36.2	322	2 PS0019	Ig gamma-2a chain
35	1102	35.9	548	2 S38864	Ig epsilon chain C
36	1092.5	35.6	327	2 S06611	Ig gamma-2 chain C
37	1082	35.2	405	1 G2MSBM	Ig gamma-2b chain
38	1066	34.7	277	2 I47162	Ig gamma 4 chain c
39	866.5	28.2	549	2 S04845	Ig heavy chain pre
40	856.5	27.9	249	2 S69340	Ig heavy chain VHI
41	820.5	26.7	241	2 S69131	Ig heavy chain (DO
42	817.5	26.6	572	2 B46529	Ig y heavy chain (
43	810	26.4	218	2 A36040	Ig heavy chain V-I
44	792	25.8	220	2 A94444	Ig gamma-1 heavy c
45	750	24.4	246	2 S38950	Ig gamma chain - m
46	745.5	24.3	213	2 S68213	Ig heavy chain (Ma
47	745	24.3	627	2 S14683	Ig mu chain precu
48	727.5	23.7	254	2 B31790	Ig heavy chain V r
49	708.5	23.1	585	2 A46507	Ig alpha chain - c
50	707	23.0	180	2 I46732	Ig gamma heavy cha
51	690	22.5	153	1 ICG12	interleukin-2 prec
52	690	22.5	153	1 ICHU2	interleukin-2 prec
53	686.5	22.4	592	2 S25705	Ig mu chain - shce
54	681	22.2	220	2 S68211	Ig heavy chain (Ma
55	666.5	21.7	568	2 A34891	Ig heavy chain pre
56	663	21.6	231	2 PC4155	Ig gamma-2b chain
57	654	21.3	577	2 I50731	Ig heavy chain - n
58	650	21.2	214	2 PC4202	monoclonal antibod
59	620	20.2	509	2 S17597	Ig delta chain (WI
60	619.5	20.2	221	2 S49220	Ig gamma-1 chain -
61	606	19.7	504	2 S00390	Ig gamma chain (cl
62	588.5	19.2	568	2 A45804	Ig mu chain C regi
63	586	19.1	143	2 S23624	Ig heavy chain V r
64	571	18.6	152	2 S14236	Ig gamma-1 chain C
65	549	17.9	342	2 A46529	Ig gamma chain (5.
66	538	17.5	170	2 A35944	Ig gamma-2a chain
67	536.5	17.5	573	2 S12838	Ig mu chain precu
68	534.5	17.4	154	2 JN0698	interleukin 2 prec
69	509.5	16.6	448	2 S03186	Ig heavy chain C r
70	501	16.3	119	2 S31107	Ig heavy chain - h
71	501	16.3	138	2 S31666	Ig heavy chain V r
72	501	16.3	160	2 S05271	Ig epsilon chain C
73	492	16.0	428	1 EHHU	Ig gamma-1 chain C
74	490	16.0	97	2 S26652	Ig variable region
75	489.5	15.9	147	2 I37780	Ig heavy chain, se
76	487	15.9	580	2 A46538	Ig heavy chain V r
77	486	15.8	119	2 D36005	Ig epsilon chain C
78	486	15.8	429	1 EHRT	Ig epsilon-chain -
79	485.5	15.8	426	2 I36948	Ig epsilon-chain - h
80	484	15.8	119	2 S31108	Ig heavy chain - h
81	483	15.7	140	2 S31686	Ig heavy chain V r
82	482.5	15.7	140	2 S70442	Ig heavy chain pre
83	482.5	15.7	155	2 S33509	interleukin-2 - Mo
84	480	15.6	123	2 S31114	Ig heavy chain - h
85	479	15.6	125	2 S30531	Ig heavy chain V r
86	478.5	15.6	154	2 S16241	interleukin-2 prec
87	477.5	15.5	124	2 S20782	Ig heavy chain V r
88	477.5	15.5	128	2 S26790	Ig heavy chain V r
89	477	15.5	1005	2 T18537	Ig heavy chain - c
90	474	15.4	119	2 C36005	Ig heavy chain V r
91	474	15.4	135	2 S31598	Ig heavy chain V r
92	474	15.4	140	2 S31588	Ig heavy chain V r
93	473.5	15.4	120	2 S48798	Ig heavy chain V r
94	470.5	15.3	118	2 S31105	Ig heavy chain (su
95	470.5	15.3	135	2 I37778	Ig variable region
96	470	15.3	119	2 S36005	Ig heavy chain V r
97	469.5	15.3	120	2 S44111	Ig heavy chain V-D
98	469.5	15.3	433	2 S31436	Ig epsilon chain -
99	469	15.3	127	2 S38489	Ig heavy chain - h
100	469	15.3	149	2 S31391	interleukin-2 prec

ALIGNMENTS

RESULT 1

GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:CROSS-references: UNIPROT:P01857; EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:CROSS-references: EMBL:Z17370
R:Rakanaishi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primärstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOI; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:CROSS-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1, 114/1, 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 57.5%; Score 1767; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.9e-92;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ASTKGPSVFPLAPSSKSTSGGTAAALCLVKGLVYPPEPVTVSWNSGALTSGVHTFPAVLQSS 179
|||||
Db 1 ASTKGPSVFPLAPSSKSTSGGTAAALCLVKGLVYPPEPVTVSWNSGALTSGVHTFPAVLQSS 60
|||||
QY 180 GLYSLSVVTVTPSSSLGTTQYICNVNHPKSTKVDKVEPKSCDKHTHTCPCPAPELGG 239
|||||
Db 61 GLYSLSVVTVTPSSSLGTTQYICNVNHPKSTKVDKVEPKSCDKHTHTCPCPAPELGG 120
|||||
QY 240 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 299
|||||
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
|||||
QY 300 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
|||||
Db 181 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
|||||
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
|||||
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
|||||
QY 420 QQGNVFCSCVMHEALHNNHYTKSLSPGK 449
|||||
Db 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330
|||||

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:CROSS-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
C:Genetics:
A:Gene: GDB:IGHG3
A:CROSS-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33

A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 53.18; Score 1630.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 3e-84;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 120 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 179
DB 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 60

QY 180 GLYSLSSVTVPPSSSLGTQYIYCNVNHKPSNTKVDKKV----- 217
DB 61 GLYSLSSVTVPPSSSLGTQYIYCNVNHKPSNTKVDKKVLTPLGDTTHTTCRCPPEPKSC 120

QY 218 -----EPKSCDKHTHTCPAPPELLGGPSVFLPFPKPKOT 252
DB 121 DTPPPCPCRPCKPSCDTPPPCPCRPCKPSCDTPPPCPCRPAPPELLGGPSVFLPFPKPKOT 180

QY 253 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 312
DB 181 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 240

QY 313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 372
DB 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRBEMTKNQVSLTCLVK 300

QY 373 GFYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCSVMHE 432
DB 301 GFYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCSVMHE 360

QY 433 ALNHHTYQKSLSPGK 449
DB 361 ALNHRTQKSLSPGK 377

RESULT 3

A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bi, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 53.0%; Score 1628.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 3.9e-84;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 120 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 179
DB 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 60

QY 180 GLYSLSSVTVPPSSSLGTQYIYCNVNHKPSNTKVDKKV----- 217
DB 61 GLYSLSSVTVPPSSSLGTQYIYCNVNHKPSNTKVDKKVLTPLGDTTHTTCRCPPEPKSC 120

QY 218 -----EPKSCDKHTHTCPAPPELLGGPSVFLPFPKPKOT 252
DB 121 DTPPPCPCRPCKPSCDTPPPCPCRPCKPSCDTPPPCPCRPAPPELLGGPSVFLPFPKPKOT 180

QY 253 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 312
DB 181 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 240

QY 313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 372
DB 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRBEMTKNQVSLTCLVK 300

QY 373 GFYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCSVMHE 432
DB 301 GFYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCSVMHE 360

QY 433 ALNHHTYQKSLSPGK 449
DB 361 ALNHRTQKSLSPGK 377

RESULT 4

G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <SLU>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.B.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, '222', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707

A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 52.2%; Score 1604; DB 1; Length 326;
Best Local Similarity 91.2%; Pred. No. 7, 7e-83;
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 120 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 179
DB 1 ASTKGPSVFPLAPSKSRSTSESTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60

QY 180 GLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239
DB 61 GLYSLSVVTPSSSFGTQTYTCNVNHPKSNTKVDKTKVERKCCV---CPPCPAPP-VAG 116

QY 240 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEOVN 299
DB 117 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEOVN 176

QY 300 STYRVSVLTVLHVDWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 177 STYRVSVLTVLHVDWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 236

QY 360 LTKNQVSLTCLVKGYFSPDIAVEWESNQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 419
DB 237 MTKNQVSLTCLVKGYFSPDIAVEWESNQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 296

QY 420 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 449
DB 297 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 51.8%; Score 1590.5; DB 1; Length 327;
Best Local Similarity 90.9%; Pred. No. 4.4e-82;
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 120 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 179
DB 1 ASTKGPSVFPLAPSKSRSTSESTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60

QY 180 GLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239
DB 61 GLYSLSVVTPSSSFGTQTYTCNVNHPKSNTKVDKRVESK---YGPCCPCPAPEFLGG 117

QY 240 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEOVN 299
DB 118 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEOVN 177

QY 300 STYRVSVLTVLHVDWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 178 STYRVSVLTVLHVDWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 237

QY 360 LTKNQVSLTCLVKGYFSPDIAVEWESNQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 419
DB 238 MTKNQVSLTCLVKGYFSPDIAVEWESNQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 297

QY 420 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 449
DB 298 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 327

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 49.1%; Score 1508.5; DB 2; Length 444;
Best Local Similarity 61.1%; Pred. No. 2.5e-77;
Matches 277; Conservative 73; Mismatches 90; Indels 13; Gaps 6;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSWVRQAPGKLEWYVIGS--SGSGST 58
DB 1 EVQVETGGGLVPGNSLKLSCLTSGFTFSNRYMHLRQPPGKRLEWIAVITVKSDNYGA 60

QY 59 YYSQSVKGRFTISRDNSKNTLYLQNRLRAEDSAVYFCTRVKLGTYFDWSQGGTLLTVS 118
DB 61 KYAESVGRFTISRDDSKSVYLMNRLREEDTATYCCRTF-WYVYAMDCWQGGTSVIVS 119

Qy	177	QSSGLYSLSVVTVPSSSLGTQTYICNVNHKSPNTKVDKKVPKSCDKTHTCPPCPAPEL	236
Db	199	QSSGLYSLSVVTVPSSSLGTQTYICNVNHKSPNTKVDKKVPKSCDKTHTCPPCPAPEL	255
Qy	237	LGSPSVFLPPPKKDTLMIISRTPEVTCVVDVSHEDBEVKFNWYVDGVEVHNATKPREE	296
Db	256	PGSPSVFIFFPKPKDTLISGTPEVTCVVDVSHEDBEVKFNWYVDGVEVHNATKPREE	315
Qy	297	QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS	356
Db	316	QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS	375
Qy	357	RDELTKNQVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTTTPVLDSDGSPFLYSKLT	414
Db	376	QBELSKVTSLSLTQVTSFYPDYIAVEQWRNGQPESEDKYGTTPQLDADSSYFLYSKLRV	435
Qy	415	DKSRWQGNVFCSCVMHEALHNNHYTKSLSLSPGK	449
Db	436	DRNSWQEGDYYTTCVMEALHNNHYTKSLSLSPGK	470
RESULT 8			
S37483			
I9 gamma-2a chain - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999			
C:Accession: S37483			
R:Ducancel, F.F.D.			
submitted to the EMBL Data Library, February 1993			
A:Reference number: S37483			
A:Accession: S37483			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-469 <DUC>			
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253			
C:Superfamily: Immunoglobulin C region; immunoglobulin homology			
C:Keywords: Immunoglobulin			
F:276-345/Domain: immunoglobulin homology <IMM>			
Query Match 46.9%; Score 1440.5; DB 2; Length 469;			
Best Local Similarity 59.1%; Pred. No. 1.7e-73;			
Matches 267; Conservative 72; Mismatches 108; Indels 5; Gaps 5;			
Qy	1	EVQLVESGGDFVQPGSLRVS CAASGFAFASHYAMSVVRQAPGKGLIEWAYISSGGSTYY	60
Db	20	QIQLOQSGPELVKPGASVKISCKASGYTFTDYINWVKQPGQGLKGIWIPASGNTKY	79
Qy	61	SDSVKGRFTISRDNSKNTLYLQWRSURPADSAYVFCRVLKLT-YTFDSWGQGTLLTVSS	119
Db	80	NENFKGKATLTVDTSSTAYMQLSSLTSDTAYVFCARAMGATATLLDYWGQGTLLTVSS	139
Qy	120	ASTKGPSVPEPLAPSSKTSGGTAALGCLVKDYPPEVPTVSNWNGALTSGVHTFPVAVLQSS	179
Db	140	AKTTAPSVTPEPLAPVCGDGTGSSVTTLGCLVKGFPEPTVLTWNSGSLSSGSHVHTFPVAVLQSD	199
Qy	180	GLYSLSVVTVPSSSLGTQTYICNVNHKSPNTKVDKKVPKSCDKTHTCPP--CPAPELL	237
Db	200	-LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVDKKIIPRG-PTIKCPCKPCAPNLL	257
Qy	238	GGPSVFLPPPKKDTLMIISRTPEVTCVVDVSHEDBEVKFNWYVDGVEVHNATKPREE	297
Db	258	GGPSVFIFFPKIKDVLMIISLSPITVCVVDVSDSDPDVQISFWPNVNEVHTAQTQTHRED	317
Qy	298	YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR	357
Db	318	YNSTLRVVSALPIQHODMWSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE	377
Qy	358	DELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS	417
Db	378	EWTKKQVTLTCNVDTDFMEDYIVVEWTNNGKTELNYKNTPEVLDSGYSFYMSYKLRVEKK	437
Qy	418	RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK	449

438 NWVERNSYSCSVH EGLHNHHTTKSF SRTPGK 469 Db

RESULT 9

S40295
IG gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Birnboim, H.C. 1993
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
A;Cross-references: UNIPROT:Q99L25
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region: immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: IG gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-95,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;32/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match	46.8%;	Score 1437;	DB 2;	Length 446;
Best Local Similarity	59.3%;	Pred. No. 2.5e-77;		
Matches	267;	Conservative	70;	Mismatches 103;
			Indels	6;
			Gaps	4;
QY	1	EVQLVESGGDFVQPG	SLRVSCAASGFAFS	HYAMSWVRQAPKGL
DB	1	QIQLOQSGPELVR	PCASVKISCKASGY	TFTDYIHWVKQRPGE
QY	61	SSVVGKRTTISRDNS	KNTLYIQMRSLRADS	AVFYCTRKLGYTFDS
DB	61	NEKFGKATLTVDTS	SSSTAYNQLSLSL	SEDSAVYFCARG--
QY	121	STKGPSVPLAPSSK	STSGGTAALGCLV	KVDFPPEPTVSWNS
DB	119	KTTASVYPLAPV	CGDTTGGSSVTI	GLCVKGYFPEPTLT
QY	181	LYSLSSVTVPSSSL	IGTQTYICNNH	KPSNTKVDKKVPEK
DB	178	LYTLSSSVTTSST	WPSOSITCNVAHP	ASSTKVDKKTLEPR
QY	239	GPSVFLPFPKDTL	MIKSTTEVTCVV	VDVSHDEPKFNWY
DB	237	GPSVFIFFPKIDV	LMISLSPWTCVV	VDVSEDDPDVQIS
QY	299	NSTRYVSVLTVL	HDWLNGKEYKCK	VSNKALPAPIEKT
DB	297	NSTRLRVSALPI	HQDWMNSGKEFK	CKVNNKDLPAPIE
QY	359	ELTKNQVSLTCL	VKGFYPSDIAV	ESWGSPENNYKTT
DB	357	EMTKQVLTCTV	DTDFMEDIV	EWNNGKELNYK
QY	419	WQQGNVFCSCVM	HEALHNHYTK	QKLSLSLSPG
DB	417	WYERNSYSCSV	VHGLHNHHTK	FSRTPG

RESULT 10

537459

Ig gamma-1 chain - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C/Accession: S31459
R/Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A/Reference number: S31459
A/Accession: S31459
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-472 <PAT>
A/Cross-references: EMBL:X69797
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: immunoglobulin
F/277-346/Domain: immunoglobulin homology <IMM>

Query Match 46.7%; Score 1434; DB 2; Length 472;
Best Local Similarity 59.4%; Pred. No. 4e-73;
Matches 274; Conservative 64; Mismatches 105; Indels 18; Gaps 5;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAAFGAFSHYAMSWVRQAPGKGLEWYAYISSGSGS--- 57
Db :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
18 QVRLOESGPSLATLLQTLSVTCTTISGFSLNNYGVDWRQAPGKALEWL----GGSGYDE 72

Qy 58 -TYSDSVKGRFTISRDNKNTLYLQMSRAEDSAVYFCRTVKLGITYY-----FDSWG 110
Db :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
73 DIDNYPVLKSRLSITKDTSKSQVSLTSTVTETDAVYCARVDYDSSHAFAYSYDFWG 132

Qy 111 QGTLLTVSSASTKGPSVFPLAPASSKSTSGGTAALCLLVCKDYFPPEPTVSNWSGALTSGVH 170
Db :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
133 PGLLI SVLSASTTPPKVPILP TSCCGDTSSIVTLGCLVSSVMPEPTVWNWSGALTSGVH 192

Qy 171 TPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHHTCPP 230
Db 193 TPFAILLQSSGLYSLSSVTVTPASTSGAQTFICNAHPASSTKVTKDRVPEPGCPDPCKHC-R 251

Qy 231 CPAPPELLGGSPSFLPPPKPKDTLMISSTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAAK 290
Db 252 CPPPELPGGSPVFIFPPPKPKDTLTISGTEPVTCVVVDVGDDPEVQFSWFVDNVEVRTAR 311

Qy 291 TKPREEQYNSTRYVVSVLTVLHQDLNGKEYCKVSKNALPAPIEKTISKAKGQPREPQV 350
Db 312 TKPREEQFNSTRVVSALPIQHODMTGKEFKCKVHNEALPAPIVRTISRTKGQAREPQV 371

Qy 351 YTIPTPSRDELTKNQVSLTCLVKGYIPSDIAVEWESNGQP--ENNYKTTTPPVLDSDGSFPL 408
Db 372 YVLAPPQEELSKSTLSVLCVLTGTFPYDPIAVEWQNGQPSEDEKYGTTTSLDADGSFYFL 431

Qy 409 YSKLTVDKSRWQQGNVPSCSVMHEALHHHYTKSLSLSPGK 449
Db 432 YSLRDKNQSQEGDITACVMMHEALHHHYTKSISKP PGK 472

RESULT 11
S69339
Ig heavy chain V region precursor - human
C/Species: Homo sapiens (man)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C/Accession: S69339; S72664
R/Khamilichl, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A/Reference number: S69339; UID:95262687; PMID:7744049
A/Accession: S69339
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-374 <KHA>
A/Cross-references: EMBL:X81695
R/Khamilichl, A.A.
submitted to the EMBL Data Library, September 1994
A/Reference number: S72664
A/Accession: S72664

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140,'C',142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 46.5%; Score 1429; DB 2; Length 374;
Best Local Similarity 62.1%; Pred. No. 5.7e-73;
Matches 282; Conservative 23; Mismatches 45; Indels 104; Gaps 4;

Qy 1 EVQLVESGGDVPQGSGSLRVSCASGAPAFSH--YAMSWVRQAQPKGLEWVAYISSGSGT 58
Db :::::|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 QITKESGPTLVTKQTILTLCTTSFGSLSKGVGVGIQPPGQALFWLALI-FWDDDK 78
Db :::::|||||:|||||:|||||:|||||:|||||:|||||:
Qy 59 YYSDSVAGRFRTISRDNSKNLTLYLMQRSIARSDSAVFCTRVKLG---TYYPDSMGQGTLL 115
Db ||:::|||||:|||||:|||||:|||||:|||||:|||||:
Qy 79 RYSPSLRTRLTIKTCKNQVVLTMVNVDPADTATYYCGYSVEGYGGYRPHSWGQGTIV 138
Db |||||:|||||:|||||:|||||:|||||:|||||:
Qy 116 TVSSASTKGPSVFPLAPSSKSTSGTAAALGLCLVKDYFPEPVTVSWNSGALTSGVHTPFAV 175
Db |||||
Qy 139 TVSS----- 142
Qy 176 LQSGLSYLSSVVTPVSSSLGTQYICNVNHKPSNTKVDKKVPEKSKDKTHTCPCPAPE 235
Db |||||-----EPKSKDKTHTCPCPAPE 160
Qy 236 LLGGSVFLFPFKPDLMISRTEPTVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
Db 161 LLGGSVFLFPFKPDLMISRTEPTVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 220
Qy 296 EQYNSTYRVVSVLTVLHODMLNGKEYCKYKSVNKAIPAEIKTISKAKGPREFQVYTLPP 355
Db 221 EQYNSTYRVVSVLTVLHODMLNGKEYCKYKSVNKAIPAEIKTISKAKGPREFQVYTLPP 280
Qy 356 SRBELTKNOVSLTCLAVGFPSDIADVSEWSNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 415
Db 281 SRBELTKNOVSLTCLAVGFPSDIADVSEWSNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 340
Qy 416 KSRWQQGNVFSVCSVMHEALNNHYTKLSLSPGK 449
Db 341 KSRWQQGNVFSVCSVMHEALNNHYTKLSLSPGK 374

RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: S25057; A02157; A26235; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
Submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A:Reference number: S25057
A:Accession: S25057
A>Status: preliminary
A:Molecule type: mRNA
A:Cross-references: UNIPROT:P01866; EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Odate, M.; Honjo, T.
Nature 283, 786-789, 1980
A>Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A:Cross-references: GB:J00461
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A>Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A:Reference number: A26235; MUID:80081501; PMID:117548
A:Contents: MPC 11

A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172,'P','174-189','FP','193-376','T','378-474 <TU1>
A>Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A>Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain C region
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172,'P','174-189','FP','193-376','T','378-474 <TU2>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A>Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b genes
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161,'L','163-189','FP','193-300','R','302-331','A','333-437','DI','440-474 <OIL>
A:CROSS-references: GB:J00461
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi,
J. Biol. Chem. 269, 12345-12350, 1994
A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967
A:Accession: A53598
A>Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
C:Genetics:
A:Introns: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers by interchain disulfide bonds. #status predicted
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F; 157-222/Domain: immunoglobulin homology <IM1>
F; 236-257/Region: hinge
F; 281-350/Domain: immunoglobulin homology <IM2>
F; 387-454/Domain: immunoglobulin homology <IM3>
F; 152/disulfide bonds: interchain (to light chain) #status predicted
F; 164-220,288-348,394-452/disulfide bonds: #status predicted
F; 247,250,253,256/disulfide bonds: interchain (to heavy chain) #status predicted
F; 324/binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	45.3%	Score 1390;	DB 1;	Length 474;
	Best Local Similarity	56.6%;	Pred. No. 1.2e-70;		
	Matches 260;	Conservative 72;	Mismatches 113;	Indels 14;	Gaps 4;
Qy	1	EVLVSEGGDFVPQGSLRVSCAAAGFAFSHYAMSWVRQAPOGKLEWAVYISGGSGTY 60			
Dd	20	EVOLQQSGPELVNPGASVKMSCKASYFTITYVMHWKPKGOGLIEWIGYNPNKDGTKP 79			
Qy	61	SDSVKGRTITSRDNSKNLTLYIQMSLRABDSAVPYCTTRVKLGTY---YPDSHGQGTLLTV 117			
Dd	80	NKPFGKATLTSDKSSNTAYMELSSLTSEDSAVVYCAR----DYDYDPFYWGQGTLTIV 135			
Qy	118	SSASTKGPSVFPLAPSSKSTSGGTGAALCLKVDKPEPVTVSWNSGALTSGVHTFPAVLQ 177			
Dd	136	SAAKTPPSVYFLAPGCCDTTGSSVTGCLVKGYFPPESVTTWMNSGSLSSVHILLSQALL 195			
Qy	178	SSGLYSLSVVTVPPSSSILGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP----- 230			
Dd	196	QSGLYTMSSTVSPTSMPSTQTVCVAHPASSITTDVKLESGLPISTINPCPPCKECKH 255			
Qy	231	CPAPELGGSPSVFLFPKPKQDTLMISRTEPTCVTVVDVSHEDPEVKFNKYVDGEVHNNAK 290			
Dd	256	CPAPNLGGSPSVTFPPENIKDLMLISLPKVTCVVVDVSDPDVQISFWFNNVEVHTAQ 315			
Qy	291	TKRREEDYSTIRYVVSVTLTVLDHQLNGKEYKCCKVNKAIPAEKTISKAKGPREPQV 350			
Dd	316	TQTHREDNSTIRVVSFLTPIQHDDMGSKFKCKVNNDKLPSIPTERTISKIIGLVRAPOV 375			
Qy	351	YTLPPSRDELTKNOVSLTCLVKGFYPSDIAEWESNGOPENNYKTTPTPVLVDSGGSFFLYS 410			

Db 376 YLLPPAQLSKQVSLCLVGFNPGLISVWTSNGHTEENYKDTAPVLDSGSGYFIYS 435
Qy 411 KLTVDKSRWQGNVFCSCVMHEALNHHYTKQSLSLSPGK 449
Db 436 KLANMTSKWEKTDSPFCNVRHEGLKKNLYLKTTISRSPGK 474
RESULT 13
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475
A:Cross-references: EMBL:X13188; NID:G51780; PIDN:CAA31580.1; PID:G51781
A:Note: This sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>
Query Match 44.5%; Score 1367.5; DB 2; Length 475;
Best Local Similarity 56.2%; Pred. No. 2,1e-69;
Matches 257; Conservative 75; Mismatches 116; Indels 9; Gaps 4;
Qy 1 EYQLVESGDFVQPGSLRVSACAAGFAPSHYAMSWVRQAPGKGLHWAYISSGSGTY 60
Db 20 QVQLQSGAELARPGASVKLSCKASGYTLTSYGISWVKRQTQGLEWIGEIVPGSGSYF 79
Qy 61 SDSVKGRTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-LGTYYPDSWGQGLTLTVSS 119
Db 80 NEKFKGKATLVDRKSSSTAYLHLSLSDSDSAVYFCAGPRQVGLLPFGYWGQGLTLVTASA 139
Qy 120 ASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 179
Db 140 AKTTPPSVYPLAPGCGDTTGSVTLGCLVKGYFPESTVTVWNSGSLSSVHTFPAVLQ-S 198
Qy 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT-HTCPP- ----CP 232
Db 199 GLYTWSSVTVPSSTWPSQTVCVAHPASSTTVDKLEPSGPTSTINPCPKCKCHKCP 258
Qy 233 APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 292
Db 259 APNLEGGPSVFIFPPNRIKDVLMISLTPTKVTCVVDVSEDDPDVQISWFNVNVVLTATQ 318
Qy 293 PREEOYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKTSKAGQPREPPQVYT 352
Db 319 THREEYNSTIRVVSALPTQHQDWLNGKGFCKVKNKDLPAPIETIISKIGLVRAPOVYI 378
Qy 353 LPSPRDELTKNQVSLTCLVKGYFPPSDIAVEVESNQGPENNYKTTTPVLDSDGSPFLYSKL 412
Db 379 LSPPEQLSRKDVSLTCLAVGSPEDISVEWTSNGHTEENYKDTAPVLDSGSGYFIYSKL 438
Qy 413 TVDKSRWQGNVFCSCVMHEALNHHYTKQSLSLSPGK 449
Db 439 NMKTSKWEKTDSPFCNVRHEGLKKNLYLKTTISRSPGK 475
RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacekovichs, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a si
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
C:Genetics:
A:Gene: IGG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 41.1%; Score 1263; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 9.4e-64;
Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;
Qy 120 ASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 179
Db 1 APKTAPSVYPLAPCSRDTSGFNVALGCLASSYFPEPTVTVWNSGALSSGVHTFPPSVLQPS 60
Qy 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239
Db 61 GLYSLSMVTVPASLSLSSKSYTCNVNHPATTTKVDKRVGTIKTKPPCPICAPACESP- ---G 116
Qy 240 PSVLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKTPREOVN 299
Db 117 PSVFIFFPKPKDTLMISRTPEVTCVVDVSOENPEVQPSVYVDGVEVHTAQTTRPKKEOFN 176
Qy 300 STYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIETKTSKAGQPREPPQVYVTLPPSPDE 359
Db 177 STYRVSVSLPTQHQDWLNGKGFCKVKNKDLPAPIETIISKAGQTRPPQVYVTLPPHAE 236
Qy 360 LTKNQVSLTCLVKGYFPPSDIAVEVESNQ- -PENNYKTTTPVLDSDGSPFLYSKLTVDKS 417
Db 237 LSRKSVSLTCLVIGFYPPDIDVEWQNGQPSPEGNRYTRTPQDDVDGTYFLYSKFSVDKA 296
Qy 418 RWQGNVFCSCVMHEALNHHYTKQSLSLSPGK 449
Db 297 SWQGGIFQCAVMHEALNHHYTKQSLSPGK 328
RESULT 15
S1866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S1866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S1866
A:Accession: S1866
A:Molecule type: mRNA
A:Residues: 1-255 <Full>
A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region
Query Match 41.0%; Score 1260; DB 4; Length 255;
Best Local Similarity 97.5%; Pred. No. 1e-63;
Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 211 TKVDKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH 270
Db 17 TVAQADVESKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH 76
Qy 271 EDPEVKFNWYVDGVEVHNATKTPREOVNSTYRVVSVLTVLHODWLNKGYKCKVSNKAL 330
Db 77 EDPEVKFNWYVDGVEVHNATKTPREOVNSTYRVVSVLTVLHODWLNKGYKCKVSNKAL 136

Qy	331	PAPIEKTISKAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE	390
Db	137		
Qy	391	NNYKTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCVMHEALHNHYTOKSLSPGK	449
Db	197		

Search completed: August 1, 2005, 09:18:43
Job time : 33.9571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 151.023 Seconds
(without alignments)
1973.408 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2223	72.4	470	2	Q6PJA4
2	2212	72.0	478	2	Q6PIA1
3	2211.5	72.0	475	2	Q6MZQ6
4	2191.5	71.4	473	2	Q6MZV7
5	2188.5	71.3	475	2	Q6GMW7
6	2187	71.2	466	2	Q6IN78
7	2187	71.2	472	2	Q6N089
8	2184.5	71.1	544	2	Q6PJ95
9	2172	70.7	480	2	Q6N094
10	2159	70.3	466	2	Q6N096
11	2158	70.3	470	2	Q7Z3W1
12	2149.5	70.0	473	2	Q6P055
13	2134	69.5	482	2	Q7Z351
14	2105.5	68.6	481	2	Q6N097
15	2083.5	67.8	469	2	Q7Z7P5
16	2064	67.2	476	2	Q6GMX1
17	2062.5	67.2	475	2	Q6N095
18	2056.5	67.0	465	2	Q6GMX6
19	2045	66.6	464	2	Q6MZU6
20	2042	66.5	480	2	Q6PJF1
21	2041.5	66.5	465	2	Q6P6C4
22	1998.5	65.1	521	2	Q8NAY9
23	1967	64.1	518	2	Q6N030
24	1955	63.7	493	2	Q68CN4
25	1945	63.3	417	2	Q6N093
26	1841	59.9	473	2	Q8TC63
27	1818	59.2	348	2	Q6PYX1
28	1812.5	59.0	476	2	Q6GMX7
29	1767	57.5	330	1	GCI_HUMAN
30	1622.5	52.8	509	2	Q8NF17
31	1604	52.2	326	1	GC2_HUMAN

32	1590.5	51.8	327	1	GC4_HUMAN
33	1538.5	50.1	471	2	Q66K04
34	1538.5	50.1	487	2	Q65ZL2
35	1530	49.8	458	2	Q65ZQ1
36	1524.5	49.6	354	2	Q86TT2
37	1521.5	49.5	473	2	Q91Z05
38	1499	48.8	464	2	Q6PIP8
39	1485.5	48.4	463	2	Q991C4
40	1477.5	48.1	473	2	Q9DBL4
41	1457	47.4	470	2	Q7TMK1
42	1452.5	47.3	465	2	Q6PJB2
43	1450	47.2	472	2	Q6PUA7
44	1436	46.8	464	2	Q6PF95
45	1409	45.9	474	2	Q8R3H6
46	1366.5	41.2	337	2	Q95M34
47	1264	41.2	679	2	Q96PQ8
48	1230.5	40.1	323	1	GC_RABIT
49	1216.5	39.6	329	1	GC2_CAVPO
50	1156	37.6	290	1	GC3_HUMAN
51	1152	37.5	326	1	GC1_RAT
52	1146.5	37.3	333	1	GCB_RAT
53	1142	37.2	324	1	GCI_MOUSE
54	1141	37.2	329	1	GC3_MOUSE
55	1139	37.1	393	1	GCIM_MOUSE
56	1130	36.8	398	1	GC3M_MOUSE
57	1126	36.7	330	1	GCAI_MOUSE
58	1123.5	36.6	335	1	GCAI_MOUSE
59	1121	36.5	399	1	GCAM_MOUSE
60	1118.5	36.4	329	1	GCC_RAT
61	1112	36.2	322	1	GCA_RAT
62	1087	35.4	336	1	GCB_MOUSE
63	1082	35.2	405	1	GCBM_MOUSE
64	901	29.3	597	2	Q96BE9
65	897.5	29.2	606	2	Q6GMV2
66	890	29.0	613	2	Q8WUK1
67	874.5	28.5	584	2	Q6INK3
68	841	27.4	585	2	Q6GFX4
69	834.5	27.2	303	2	Q6KAM2
70	833	27.1	493	2	Q6GMX2
71	823.5	26.8	494	2	Q96K68
72	813	26.5	593	2	Q6INM5
73	812	26.4	487	2	Q99KA4
74	812	26.4	614	2	Q6DDQ7
75	810	26.4	493	2	Q8NCL6
76	802	26.1	479	2	Q6MZV6
77	801	26.1	487	2	Q6ZVX0
78	799	26.0	499	2	Q8NSK4
79	794.5	25.9	486	2	Q91Z07
80	790	25.7	479	2	Q91WP5
81	788	25.7	483	2	Q6MZB8
82	784	25.5	485	2	Q6PDB8
83	772.5	25.2	494	2	Q6ZM64
84	769	25.0	519	2	Q6N092
85	764	24.9	480	2	Q91XE1
86	762.5	24.8	484	2	Q8VEA0
87	760	24.7	487	2	Q8OZ17
88	757	24.6	613	2	Q8VXC7
89	752.5	24.5	614	2	Q7TMT6
90	727	23.7	597	2	Q6GMX5
91	727	23.7	597	2	Q6N010
92	721	23.5	498	2	Q6N041
93	721	23.5	597	2	Q9BQB8
94	715.5	23.3	595	2	Q8WUX4
95	715.5	23.3	625	2	Q96AA6
96	713.5	23.2	500	2	Q6N091
97	707.5	23.0	500	2	Q9BRV0
98	705	22.9	620	2	Q96EY0
99	703.5	22.9	480	2	Q6P089
100	699	22.8	497	2	Q8WY24

ALIGNMENTS

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RESULT 1
Q6PJA4 ID Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC O6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 72.4%; Score 2223; DB 2; Length 470;
Best Local Similarity 93.1%; Pred. No. 1.8e-136;
Matches 420; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVQLVESGGDFVQPGSLRVS CAASGFARFASHYAMSVRQAPGKLEWYAYISGSGSTYY 60
DB 20 EVQLVESGGGLVQPGSLRLSCVSGFTFSYWMNSVVRQAPGKLEWANIIRKQDSEKYY 79
QY 61 SDSVKGRFTISRDNSKNTLYLQWRSIRLAEDSAVYFCTRVKLGTG--YFDSWQGGTLLTVS 118
DB 80 VDSVKGRFTISRDNAKNSLYLQWNSIRLAEDTAVYVCARDGSSWYRDWDPWQGGTLTVS 139
QY 119 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKCLVDPFPPVTVSNVNSGALTSGVHTFPAVLQS 178
DB 140 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKCLVDPFPPVTVSNVNSGALTSGVHTFPAVLQS 199

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DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 72.0%; Score 2212; DB 2; Length 478;
Best Local Similarity 91.3%; Pred. No. 9.5e-136;
Matches 419; Conservative 10; Mismatches 20; Indels 10; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSACASGFAPSHYAMSVVRQAPGKLEWVAIVISGGSGTYY 60
DB 20 EVOLVESGGGLVPGGSLRVSACASGFTFSYMSWVRQAPGKLEWVAIKDGSKYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTR-----VKLGTYF--DSWG 110
DB 80 VDSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCAREFESTMTTNNADYYFYMDVWG 139
QY 111 QGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVH 170
DB 140 KGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVH 199
QY 171 TPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPP 230
DB 200 TFAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPP 259
QY 231 CPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 290
DB 260 CPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 319
QY 291 TKPREEQNSTYRVSVLTVLHQDLNGLKEYCKYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
DB 320 TKPREEQNSTYRVSVLTVLHQDLNGLKEYCKYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYS 410
DB 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYS 439
QY 411 KLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 449
DB 440 KLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 478

RESULT 3
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFp686G11190.
GN Name=DKFp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 72.0%; Score 2211.5; DB 2; Length 475;
Best Local Similarity 91.2%; Pred. No. 1e-135;
Matches 416; Conservative 13; Mismatches 20; Indels 7; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSACASGFAPSHYAMSVVRQAPGKLEWVAIVISGGSGTYY 60
DB 20 EVOLVESGGGLVPGGSLRVSACASGFTFRYAMSVVRQAPGKLEWVSGISSGVNTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-----YFDSMQGT 113
DB 80 ADSVKGRFTISGDISNTLYLQMRSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139
QY 114 LITVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFP 173
DB 140 LVSVAASASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFP 199
QY 174 AVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPA 233
DB 200 AVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPA 259
QY 234 PELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
DB 260 PELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319
QY 294 REEQNSTYRVSVLTVLHQDLNGLKEYCKYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
DB 320 REEQNSTYRVSVLTVLHQDLNGLKEYCKYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379
QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYSKLT 413
DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYSKLT 439
QY 414 VDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 449
DB 440 VDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 475

RESULT 4
Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFp686C11235.
GN Name=DKFp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

Query Match 71.4%; Score 2191.5; DB 2; Length 473;
Best Local Similarity 90.1%; Pred. No. 28-134;
Matches 409; Conservative 21; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSQAAGFAFVSHYAMVWVRQAPGKLEWYVYSSGGSGTY 60
DB 20 ELQLVESGGGLVQPGGSLRLSCAASGFTFSFEMVWVRQAPGKLEWYVYSSGNVY 79
QY 61 SDVSKGRFTISRDNSKNTLYIQMRSLRAEDSAVFCTRVKLT-----YFDSWQGGTLL 115
DB 80 ADSLQGRFTISRDNARNSLYLQWNSLRAEDTAVYICARQNEHTSPWYPSFFDYWGQGLIV 139
QY 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPEPTVTVSNWNGALTSGVHTPEAV 175
DB 140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSNWNGALTSGVHTFPV 199
QY 176 LQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPE 235
DB 200 LQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPE 259
QY 236 LLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
DB 260 LLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319
QY 296 EGYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPP 355
DB 320 EGYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPP 379
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 415
DB 380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 439
QY 416 KSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 449
DB 440 KSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 473

RESULT 5
Q6GMW7 PRELIMINARY; PRT; 475 AA.
ID Q6GMW7
AC Q6GMW7
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzynowski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.C1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 71.3%; Score 2188.5; DB 2; Length 475;
Best Local Similarity 91.0%; Pred. No. 3.2e-134;
Matches 415; Conservative 11; Mismatches 23; Indels 7; Gaps 2;

QY 1 EVQLVESGGDFVQPGGSLRVSQAAGFAFVSHYAMVWVRQAPGKLEWYVYSSGGSGTY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVASFYLSRHAHWVRQAPGKLEWYVYSSGNSENSTY 79
QY 61 SDVSKGRFTISRDNSKNTLYIQMRSLRAEDSAVFCTRVK-----LGYT- FDSWQGT 113
DB 80 ADSVSKGRFTISRDNYKNTLYLQGLSLRAEDKAVYICARCRGDTCLNFFYGLDVGQGT 139
QY 114 LLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPEPTVTVSNWNGALTSVHTFP 173
DB 140 TVIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPEPTVTVSNWNGALTSVHTFP 199
QY 174 AVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPA 233
DB 200 AVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPA 259
QY 234 PELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
DB 260 PELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319
QY 294 REEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL 353
DB 320 REEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL 379
QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 413
DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 439
QY 414 VDKSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 449
DB 440 VDKSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 475

RESULT 6
Q6IN78 PRELIMINARY; PRT; 466 AA.
ID Q6IN78
AC Q6IN78
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villaflora D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallos D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC072419; AAH72419.1; --
DR HSSP; P01861; IADQ
DR InterPro; IPR003599; Ig_
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDEB81076E CRC64;

Query Match 71.2%; Score 2187; DB 2; Length 466;
Best Local Similarity 92.0%; Pred. No. 3.9e-134;
Matches 415; Conservative 11; Mismatches 19; Indels 6; Gaps 3;

QY 1 EVQLVESGGDFVQPQGSLRVSCAASGPAFSAHYAMSVWRQAAPKGLEWVAIVYSSGSSTYY 60
DQ 20 EVQLVESGGGLTQPQSGSLTLCAASGLTVSSNMHWVRQAAPKGLEWSVLVIGGA-TYY 78

QY 61 SDSVKGRFTISRDNCKNTLYLQMRSIRAEADSAYVFCTRKVLGT---NGOQTLLTVS 118
DQ 79 ADSVKGRFTISRDNCKNTLYLQMSLRAREDTAVYCARN--GNVVVPAAHPGGQGLTVTS 135

QY 119 SSTTKGPSVFPPLAPSFKTSKSTSGTAALGLVDKYFPEPVTVSNMGALTSGVHTPPAVLQS 178
DQ 136 SSTTKGPSVFPPLAPSFKTSKSTSGTAALGLVDKYFPEPVTVSNMGALTSGVHTPPAVLQS 195

QY 179 SGILYSLSVVTPVPSLSLTQTICNVNKPNSNTKVKKVEPKSCDKTHTCPCPAPELLG 238
DQ 196 SGILYSLSVVTPVPSLSLTQTICNVNKPNSNTKVKKVEPKSCDKTHTCPCPAPELLG 255

QY 239 GPSVFLFPKPKDITLMISRTPEVTCCVVDDSHEDPEVKFNMYVDGVEVHNNAKTKEEQY 298
DQ 256 GPSVFLFPKPKDITLMISRTPEVTCCVVDDSHEDPEVKFNMYVDGVEVHNNAKTKEEQY 315

QY 299 NSTYRVSVLTVLHQDWLNKGKEYCKVSKNALPAPIEKTIISKAKGPQREPOVYTLPSPSRD 358

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Db 319 EYNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGPPEQVYTLPP 378
QY 356 SRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVD 415
Db 379 SRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVD 438
QY 416 KSRWQOGNVFSCVSMHEALHNNHYTKQSLSLSPGK 449
Db 439 KSRWQOGNVFSCVSMHEALHNNHYTKQSLSLSPGK 472

RESULT 8
Q6PJ95 PRELIMINARY; PRT; 544 AA.
AC Q6PJ95;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;
```

Query Match 71.1%; Score 2184.5; DB 2; Length 544;
Best Local Similarity 87.4%; Pred. No. 7e-134;
Matches 418; Conservative 12; Mismatches 29; Indels 19; Gaps 2;

```
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGPAFASHVAMSWVRQAQPGKLEWVAYISSGGSGTY 60
Db 20 QAQLVESGGGVVQPGSSLRSLCAASGFRFSYGMHWVRQAQPGKLEWVAVFSYDSDDKY 79
QY 61 SDSVKGREFTISRDNSKNTLYLQMSRLRAEDSAVYFCTRVKLTGY-----YFSWGGQT 113
Db 80 AASVKGREFTISRDNSKNTLSLQMSRLRVEDTAVVYCAKDQKPMWYNSWFLTNFDSWGRGT 139
QY 114 LLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFP 173
Db 140 LVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFP 199
QY 174 AVLQSSGLYSLSSVTVVFPSSSLGTQTYICNNHNPSTNTKDKKVPKPKCDKTHTCPPCPA 233
Db 200 AVLQSSGLYSLSSVTVVFPSSSLGTQTYICNNHNPSTNTKDKKVPKPKCDKTHTCPPCPA 259
QY 234 PELLGGPSVFLPPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
Db 260 PELLGGPSVFLPPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319
QY 294 REEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGPREPVYTL 353
Db 320 REEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGPREPVYTL 379
QY 354 PPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 413
Db 380 PPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 439
QY 414 VDKSRWQOGNVFSCVSMHEALHNNHYTKQSLSLSPGKAPTSSSTKTKTQLQLEHLLDLQ 471
Db 440 VDKSRWQOGNVFSCVSMHEALHNNHYTKQSLSLSP-----ELQLBESCAEAQ 485

RESULT 9
Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein DKFPz686001196.
GN Name=DKFPz686001196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 252612 MW; 225247F3D35AEC18 CRC64;
```

Query Match 70.7%; Score 2172; DB 2; Length 480;
Best Local Similarity 88.1%; Pred. No. 3.8e-133;
Matches 406; Conservative 21; Mismatches 22; Indels 12; Gaps 1;


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QY 1 EVOLVESGDFVQPGGSLRVSCAASGPAFASHYAMSVWRQAPGKGLVWVAVISSGGSTYY 60
Db 20 EEELVESGGGLVQPGGSLRLSCAASGFTFRSFMNVRQAPGKGLVWVAVINSRGNEKYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTYYTYPDSGOGTLTVSSA 108
Db 80 GESVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTYYTYPDSGOGTLTVSSA 139
QY 109 WGQGTLLTVSSASTKGPSVFLPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTS 168
Db 140 WGQGTLLTVSSASTKGPSVFLPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTS 199
QY 169 VHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVPKSCDKTHTC 228
Db 200 VHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVPKSCDKTHTC 259
QY 229 PPCPAPELLGGPSVFLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288
Db 260 PPCPAPELLGGPSVFLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319
QY 289 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 348
Db 320 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 379
QY 349 QVTVLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 408
Db 380 QVTVLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 439
QY 409 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 449
Db 440 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 480
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RESULT 10

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Q6N096 ID Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKF2p686I15196.
GN Name=DKF2p686I15196;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAE45774.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;
```

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Query Match 70.1%; Score 2159; DB 2; Length 466;
Best Local Similarity 90.8%; Pred. No. 2.6e-132;
Matches 407; Conservative 16; Mismatches 24; Indels 2; Gaps 1;
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RESULT 11

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Q7Z5W1 ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoeh P.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 32.5277 seconds
(without alignments)
1284.140 Million cell updates/sec

Title: US-10-089-500-54
Perfect score: 568
Sequence: 1 DIQWTQSPSLASVGRVT.....HQYSKLPWTFQGQTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	100.0	108	4	AAB81988
2	568	100.0	128	4	AAB81999
3	562	98.9	108	6	ABU11011
4	561	98.8	128	4	AAB81994
5	555	97.7	128	4	AAB81997
6	551	97.0	128	4	AAB81993
7	548	96.5	108	4	AAB81986
8	545	96.0	128	4	AAB81995
9	544	95.8	128	4	AAB81996
10	545	95.8	128	4	AAB81998
11	532	93.7	128	4	AAB81992
12	514	90.5	108	4	AAB81990
13	514	90.5	108	6	ABU11013
14	514	90.5	128	3	AAB01628
15	514	90.5	128	4	AAB81978
16	514	90.5	128	6	ABU11003
17	513	90.3	128	2	AAR33257
18	507	89.3	110	2	AAW70673
19	507	89.3	110	5	ABP61242
20	507	89.3	237	2	AAW70703
21	507	89.3	650	5	ABP61241
22	506	89.1	128	2	AAW728368
23	505	88.9	107	2	AAW68805
24	505	88.9	107	2	AAW70625
25	505	88.9	107	5	ABP61194

99 480 84.5 246 8 ADH50846 AaH50846 SGIV RPB4
100 480 84.5 256 3 AAY55072 Aay55072 Interleuk

ALIGNMENTS

RESULT 1

AAAB81988
ID AAB81988 standard; protein; 108 AA.
AC AAB81988;
XX
XX 03-JUL-2001 (first entry)
DT
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX

XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

XX Claim 22; Page 172-173; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 568; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60
DB |||||
1 DIQMTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60
QY 61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFQGQTKVEIKR 108
DB |||||
61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFQGQTKVEIKR 108

RESULT 2

AAAB81999
ID AAB81999 standard; protein; 128 AA.
XX
AC AAB81999;
XX
XX 03-JUL-2001 (first entry)
DT
XX

DE Ganglioside GD3 specific antibody related protein #8.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
DR N-PSDB; AAF86913.

XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

XX Example 1; Page 166; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX SQ Sequence 128 AA;

Query Match 100.0%; Score 568; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60
DB |||||
21 DIQMTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFQGQTKVEIKR 108
DB |||||
81 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFQGQTKVEIKR 128

RESULT 3

ABU11011
ID ABU11011 standard; protein; 108 AA.
XX
AC ABU11011;
XX
XX 04-FEB-2003 (first entry)
DT
XX
XX Modified ganglioside GD3 antibody associated protein #4.
DE
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
KW Ganglioside; GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS Synthetic.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-JP003170.
PF
XX 29-MAR-2001; 2001JP-00097483.
PR
XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX Shitara K, Niwa R, Kanazawa J, Aaada M;
 XX WPI; 2003-067410/06.
 XX
 XX Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX
 XX Claim 8; Page 100; 121pp; Japanese.
 XX
 XX The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 XX
 XX Sequence 108 AA;

Query Match 98.9%; Score 562; DB 6; Length 108;
 Best Local Similarity 99.1%; Pred. No. 3.6e-35;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAPKLLIFYSNHLHSGVPS 60
 QY 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGTKVEIKR 108
 DB 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGTKVEIKR 108

RESULT 4
 AAB81994
 ID AAB81994 standard; protein; 128 AA.
 XX
 XX AAB81994;
 XX
 XX 03-JUL-2001 (first entry)
 XX Ganglioside GD3 specific antibody related protein #3.
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
 XX Cancer.
 XX Synthetic.
 XX WO200123432-A1.
 XX
 XX 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000WO-JP006774.
 XX
 XX 30-SEP-1999; 99JP-00278291.
 XX 06-APR-2000; 2000JP-00105088.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266143/27.
 XX N-PSDB; AAF86898.
 XX
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 XX Example 1; Page 155-156; 183pp; Japanese.

XX
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX
 XX Sequence 128 AA;
 Query Match 98.8%; Score 561; DB 4; Length 128;
 Best Local Similarity 98.1%; Pred. No. 5e-35;
 Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 60
 DB 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 80
 QY 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGTKVEIKR 108
 DB 81 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGTKVEIKR 128

RESULT 5
 AAB81997
 ID AAB81997 standard; protein; 128 AA.
 XX
 XX AAB81997;
 XX
 XX 03-JUL-2001 (first entry)
 XX Ganglioside GD3 specific antibody related protein #6.
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
 XX cancer.
 XX Synthetic.
 XX WO200123432-A1.
 XX
 XX 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000WO-JP006774.
 XX
 XX 30-SEP-1999; 99JP-00278291.
 XX 06-APR-2000; 2000JP-00105088.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266143/27.
 XX N-PSDB; AAF86907.
 XX
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 XX Example 1; Page 161-162; 183pp; Japanese.

XX
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX
 XX Sequence 128 AA;
 Query Match 97.7%; Score 555; DB 4; Length 128;
 Best Local Similarity 98.1%; Pred. No. 1.4e-34;
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 60

```
Db      21 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQPKAPKLLIFYSNLSHGVP 80
QY      61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGQTKVEIKR 108
Db      81 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGQTKVEIKR 128

RESULT 6
AAB81993
ID AAB81993 standard; protein; 128 AA.
XX
AC AAB81993;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein #2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 153; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 97.0%; Score 551; DB 4; Length 128;
Best Local Similarity 97.2%; Pred. No. 2.8e-34;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQPKAPKLLIFYSNLSHGVP 60
Db 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQPKAPKLLIFYSNLSHGVP 80
QY 61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGQTKVEIKR 108
Db 81 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGQTKVEIKR 128

RESULT 7
AAB81986
ID AAB81986 standard; protein; 108 AA.
XX
AC AAB81986;
XX
```

```
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 143-144; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match 96.5%; Score 548; DB 4; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.1e-34;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQPKAPKLLIFYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQPKAPKLLIFYSNLSHGVP 60
QY 61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGQTKVEIKR 108
Db 61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGQTKVEIKR 108

RESULT 8
AAB81995
ID AAB81995 standard; protein; 128 AA.
XX
AC AAB81995;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein #4.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
```


PR 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266143/27.
 DR N-PSDB; AAF86901.
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 XX Example 1; Page 157-158; 183pp; Japanese.
 PS
 PS The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 XX Sequence 128 AA;
 SQ
 Query Match 96.0%; Score 545; DB 4; Length 128;
 Best Local Similarity 95.4%; Pred. No. 8e-34;
 Matches 103; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60
 DB 21 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 80
 QY 61 RFSGGSGSDTYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 108
 DB 81 RFSGGSGSDTYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 128
 RESULT 9
 AAB81996
 ID AAB81996 standard; protein; 128 AA.
 XX
 AC AAB81996;
 XX
 XX 03-JUL-2001 (first entry)
 DT
 XX Ganglioside GD3 specific antibody related protein #5.
 DE
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KW cancer.
 KW
 OS Synthetic.
 OS
 XX WO200123432-A1.
 PN
 XX 05-APR-2001.
 PD
 XX 29-SEP-2000; 2000WO-JP006774.
 PF
 XX 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266143/27.
 DR N-PSDB; AAF86904.
 XX
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.

XX Example 1; Page 159-160; 183pp; Japanese.
 XX
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 XX Sequence 128 AA;
 SQ
 Query Match 96.0%; Score 545; DB 4; Length 128;
 Best Local Similarity 95.4%; Pred. No. 8e-34;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60
 DB 21 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 80
 QY 61 RFSGGSGSDTYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 108
 DB 81 RFSGGSGSDTYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 128
 RESULT 10
 AAB81998
 ID AAB81998 standard; protein; 128 AA.
 XX
 AC AAB81998;
 XX
 XX 03-JUL-2001 (first entry)
 DT
 XX Ganglioside GD3 specific antibody related protein #7.
 DE
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KW cancer.
 KW
 OS Synthetic.
 OS
 XX WO200123432-A1.
 PN
 XX 05-APR-2001.
 PD
 XX 29-SEP-2000; 2000WO-JP006774.
 PF
 XX 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266143/27.
 DR N-PSDB; AAF86912.
 XX
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 XX Example 3; Page 164-165; 183pp; Japanese.
 PS
 PS The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 XX Sequence 128 AA;
 SQ
 Query Match 95.8%; Score 544; DB 4; Length 128;
 Best Local Similarity 96.3%; Pred. No. 9.5e-34;
 Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 60
DB 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 80
QY 61 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 108
DB 81 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 128

RESULT 11
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
AC AAB81992;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #1.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 11; Page 150-151; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 93.7%; Score 532; DB 4; Length 128;
Best Local Similarity 93.5%; Pred. No. 7.7e-33;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 60
DB 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 80
QY 61 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 108
DB 81 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 128

RESULT 12
AAB81990
ID AAB81990 standard; protein; 108 AA.
XX
AC AAB81990;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 11; Page 174-175; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match 90.5%; Score 514; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.5e-31;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 60
QY 61 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 13
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
AC AAB81992;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #1.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 11; Page 174-175; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match 90.5%; Score 514; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.5e-31;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSNLSHGVPVS 60
QY 61 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGGTDYTLTITSSLPEDFATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 13
AAB81990
ID AAB81990 standard; protein; 108 AA.
XX
AC AAB81990;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #6.
XX
KW Ganglioside GD3; anti-ganglioside GD3 antibody associated protein #6.
XX
OS Mus musculus.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-JP003170.
```

XX PR 29-MAR-2001; 2001JP-00097483.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX PR WPI; 2003-067410/06.
 XX
 XX Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX
 XX Claim 7; Page 113; 121pp; Japanese.
 XX
 XX The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 XX
 XX Sequence 108 AA;
 SQ
 Query Match 90.5%; Score 514; DB 6; Length 108;
 Best Local Similarity 88.9%; Pred. No. 1.5e-31;
 Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPDKAVKLLIFYSSNLHSGVPS 60
 DB 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
 QY 61 RFSGGSGTDYTLTISLQPEDTATYFCHQYSKLPWTFGGGTKEIKR 108
 DB 61 RFSGGSGTDYSLTISNLEPEDTATYFCHQYSKLPWTFGGGTKEIKR 108
 RESULT 14
 AAB01628
 ID AAB01628 standard; protein; 128 AA.
 XX
 XX AAB01628;
 XX
 XX 07-DEC-2000 (first entry)
 XX
 XX Murine immunoglobulin light chain variable region.
 XX
 XX Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
 XX humanised antibody.
 XX
 XX Mus sp.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..20
 XX /label= signal_peptide
 XX Protein 21..128
 XX /label= mature_immunoglobulin_light_chain_v_region
 XX
 XX EP1013761-A2.
 XX
 XX 28-JUN-2000.
 XX
 XX 18-SEP-1992; 99EP-00124345.
 XX
 XX 18-SEP-1991; 91JP-00238375.
 XX
 XX 18-SEP-1992; 92EP-00116026.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
 XX

DR WPI; 2000-402204/35.
 DR N-PSDB; AAA51004.
 XX
 XX New humanized chimera antibody KM-871 useful for treating cancer,
 PT comprises variable region of mouse monoclonal antibody, reactive with
 PT ganglioside and human antibody constant region.
 XX
 XX Claim 14; Page 28-29; 65pp; English.
 XX
 XX The present sequence is a murine immunoglobulin light chain variable
 CC region from plasmid KM-641. The coding sequence was used in the creation
 CC of an expression vector, along with the sequence for a human antibody, to
 CC produce humanised chimaeric antibodies, which can be used to treat
 CC cancer. Humanised chimaeric antibodies are more effective than mouse
 CC antibodies as they do not provoke a reaction in the human and side
 CC effects, such as the formation of anti-mouse immunoglobulin antibody and
 CC the rapid half-life of the immunoglobulins, do not occur
 XX
 XX Sequence 128 AA;
 SQ
 Query Match 90.5%; Score 514; DB 3; Length 128;
 Best Local Similarity 88.9%; Pred. No. 1.8e-31;
 Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPDKAVKLLIFYSSNLHSGVPS 60
 DB 21 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 80
 QY 61 RFSGGSGTDYTLTISLQPEDTATYFCHQYSKLPWTFGGGTKEIKR 108
 DB 81 RFSGGSGTDYSLTISNLEPEDTATYFCHQYSKLPWTFGGGTKEIKR 128
 RESULT 15
 AAB81978
 ID AAB81978 standard; protein; 128 AA.
 XX
 XX AAB81978;
 XX
 XX 03-JUL-2001 (first entry)
 XX
 XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
 XX
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
 XX cancer.
 XX
 XX Mus musculus.
 XX
 XX WO200123432-A1.
 XX
 XX 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000WO-JP006774.
 XX
 XX 30-SEP-1999; 99JP-00278291.
 XX
 XX 06-APR-2000; 2000JP-00105088.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX
 XX WPI; 2001-266143/27.
 XX
 XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 XX Example 1; Page 140; 183pp; Japanese.
 XX
 XX The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumours, particularly cancer
 CC

CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

CC of the invention

XX

SQ Sequence 128 AA;

Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.8e-31;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSSNLHSGVPS 60

Db 21 DIQMTQTASSLPASLGDRVTTCSSASQDISNLYNWYQQKPDGTVKLLIFYSNNLHSGVPS 80

QY 61 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108

Db 81 RFSGGGSTDYSLTISNLEPEDIATYFCHOYKLPWTFGGTKLEIKR 128

Search completed: August 1, 2005, 09:10:09
Job time : 33.5277 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 8.19913 Seconds
(without alignments)
983.287 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfileesi.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	514	90.5	128	4	US-09-764-304-10
4	514	90.5	128	4	US-09-764-304-19
5	507	89.3	491	4	US-10-011-125A-2
6	503	88.6	110	4	US-09-440-781-94
7	491	86.4	108	3	US-09-865-059-3
8	487	85.7	127	3	US-08-649-100-33
9	484	85.2	114	1	US-08-458-516-12
10	481	84.7	110	4	US-09-440-781-95
11	480	84.5	107	2	US-07-934-373C-17
12	480	84.5	107	2	US-08-652-558-2
13	480	84.5	107	3	US-08-437-642B-17
14	480	84.5	107	4	US-08-146-206C-17
15	480	84.5	107	4	US-09-705-686-17
16	480	84.5	107	4	US-09-705-392A-17
17	480	84.5	107	4	US-09-705-398-17
18	480	84.5	107	5	PCT-US93-07832-17
19	480	84.5	109	3	US-07-934-373C-47
20	480	84.5	109	3	US-08-437-642B-47
21	480	84.5	214	2	US-07-934-373C-40
22	480	84.5	214	2	US-08-788-800-11
23	480	84.5	214	3	US-08-437-642B-40
24	480	84.5	214	3	US-09-097-309-2
25	480	84.5	214	3	US-09-097-171A-2
26	480	84.5	214	3	US-09-460-587-2
27	480	84.5	214	4	US-09-940-166A-2
28	480	84.5	214	5	PCT-US93-07832-40
29	480	84.5	233	2	US-07-934-373C-25
30	480	84.5	233	2	US-08-437-642B-25
31	480	84.5	233	4	US-08-146-206C-25
32	480	84.5	233	4	US-09-705-686-25
33	480	84.5	233	4	US-09-705-392A-25
34	480	84.5	233	4	US-09-705-398-25
35	480	84.5	233	5	PCT-US93-07832-25
36	480	84.5	237	3	US-09-097-309-6
37	480	84.5	237	3	US-09-097-171A-10
38	480	84.5	237	3	US-09-422-712B-2
39	480	84.5	237	3	US-09-607-756-2
40	480	84.5	237	3	US-09-460-587-6
41	480	84.5	237	1	US-08-940-166A-6
42	479	84.3	107	1	US-08-458-516-8
43	476	83.8	107	3	US-09-254-189-1
44	475	83.6	108	3	US-08-974-899-3
45	475	83.6	108	4	US-09-795-798-3
46	475	83.6	111	1	US-08-137-117D-67
47	475	83.6	111	1	US-08-436-717-67
48	475	83.6	126	1	US-08-137-117D-71
49	475	83.6	126	2	US-08-436-717-71
50	472	83.1	214	2	US-07-934-373C-39
51	472	83.1	214	3	US-08-437-642B-39
52	472	83.1	214	5	PCT-US93-07832-39
53	470	82.7	107	3	US-07-934-373C-18
54	470	82.7	107	3	US-08-437-642B-18
55	470	82.7	107	4	US-08-146-206C-18
56	470	82.7	107	4	US-09-648-067A-14
57	470	82.7	107	4	US-09-705-686-18
58	470	82.7	107	4	US-09-705-392A-18
59	470	82.7	107	4	US-09-705-398-18
60	470	82.7	107	5	PCT-US93-07832-18
61	468	82.4	107	2	US-08-652-558-35
62	466	82.0	109	2	US-07-934-373C-3
63	466	82.0	109	3	US-08-437-642B-3
64	466	82.0	109	4	US-08-146-206C-3
65	466	82.0	109	4	US-09-705-686-3
66	466	82.0	109	4	US-09-705-392A-3
67	466	82.0	109	4	US-09-705-398-3
68	466	82.0	109	5	PCT-US93-07832-3
69	465	81.9	105	3	US-09-199-149-31
70	465	81.9	212	4	US-10-011-125A-5
71	464	81.7	109	4	US-09-386-658A-4
72	463	81.5	109	4	US-09-802-083-4
73	462	81.3	107	2	US-08-318-157B-6
74	462	81.3	107	4	US-09-253-794-6
75	462	81.3	109	3	US-09-157-370-3
76	461	81.2	131	1	US-08-236-520-2
77	461	81.2	131	5	PCT-US95-05262-2
78	460	81.1	114	2	US-08-561-521-43
79	460	81.1	114	5	PCT-US95-01219-43
80	458	80.6	127	4	US-09-809-733-10
81	457	80.5	112	3	US-08-487-761-13
82	456	80.3	102	3	US-09-199-149-10
83	456	80.3	102	3	US-09-199-149-29
84	456	80.3	108	2	US-08-070-116A-7
85	456	80.3	108	2	US-08-116-247-9
86	456	80.3	108	3	US-08-199-143-14
87	456	80.3	108	4	US-08-557-050-7
88	456	80.3	108	4	US-08-454-899G-100
89	456	80.3	108	3	US-09-348-224-9
90	455	80.1	108	3	US-09-025-769B-14
91	455	80.1	108	4	US-09-490-070A-14
92	455	80.1	108	4	US-09-490-153-14
93	455	80.1	108	4	US-09-490-324-14
94	453	79.8	108	3	US-08-602-725-29
95	453	79.8	108	3	US-09-199-149-7
96	452	79.6	107	1	US-08-458-516-9
97	452	79.6	107	2	US-08-561-521-6
98	452	79.6	107	2	US-08-652-558-34
99	452	79.6	107	3	US-09-025-203-15
100	452	79.6	107	4	US-09-999-021-15

ALIGNMENTS

```
RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-09-225-322B-10

Query Match          90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.3e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNMYQQKPKAVKLLIFYSNLSHGVP 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNVLNMYQQKPKDGTVKLLIFYSNLSHGVP 80
QY 61 RFGSGSGTDTLTITSSLPEDIAFYFCHQYKSLPWTFGQGTKEIKR 108
DB 81 RFGSGSGTDTLTITSSLPEDIAFYFCHQYKSLPWTFGGKLEIKR 128

RESULT 2
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cdna KM-641
US-09-764-304-10

Query Match          90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.3e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNMYQQKPKAVKLLIFYSNLSHGVP 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNVLNMYQQKPKDGTVKLLIFYSNLSHGVP 80
QY 61 RFGSGSGTDTLTITSSLPEDIAFYFCHQYKSLPWTFGQGTKEIKR 108
DB 81 RFGSGSGTDTLTITSSLPEDIAFYFCHQYKSLPWTFGGKLEIKR 128

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
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Db 81 RFGSGSGTDYLTISNLEPDIATVFCQYSKLPMTFGGTKLEIKR 128

RESULT 4

US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.3e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60
Db 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 80
QY 61 RFGSGSGTDYLTISNLEPDIATVFCQYSKLPMTFGGTKLEIKR 108
Db 81 RFGSGSGTDYLTISNLEPDIATVFCQYSKLPMTFGGTKLEIKR 128

RESULT 5

US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121

US-10-011-125A-2

Query Match 89.3%; Score 507; DB 4; Length 491;
Best Local Similarity 88.0%; Pred. No. 2.9e-42;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 83
QY 61 RFGSGSGTDYLTISNLEPDIATVFCQYSKLPMTFGGTKLEIKR 108
Db 84 RFGSGSGTDYLTISNLEPDIATVFCQYSKLPMTFGGTKLEIKR 131

RESULT 6

US-09-440-781-94
; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-Yee Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match 88.6%; Score 503; DB 4; Length 110;
Best Local Similarity 87.0%; Pred. No. 1.3e-42;
Matches 94; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60
QY 61 RFGSGSGTDYLTISNLEPDIATVFCQYSKLPMTFGGTKLEIKR 108
Db 61 RFGSGSGTDYLTISNLEPDIATVFCQYSKLPMTFGGTKLEIKR 108

RESULT 7

US-09-065-059-3
; Sequence 3, Application US/09065059
; Patent No. 6088841
; GENERAL INFORMATION:
; APPLICANT: SEINO, Ken-ichiro
; APPLICANT: KAYAGAKI, No. 6068841uhiko
; APPLICANT: YAGITA, Hideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

Db 61 RFGSGSGDTYLTITSSLPDDFATYFCQQGNTLPWTFGGQTKVEIKR 108

RESULT 10

US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632326
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain

US-09-440-781-95
Query Match 84.7%; Score 481; DB 4; Length 110;
Best Local Similarity 81.5%; Pred. No. 2e-40;
Matches 88; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60
Qy 61 RFGSGSGDTYLTITSSLPDDFATYFCQQGNTLPWTFGGQTKVEIKR 108
Db 61 RFGSGSGDTYLTITSSLPDDFATYFCQQGNTLPWTFGGQTKVEIKR 108

RESULT 11

US-07-934-373C-17
; Sequence 17, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-17

Query Match 84.5%; Score 480; DB 2; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.5e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60
Qy 61 RFGSGSGDTYLTITSSLPDDFATYFCQQGNTLPWTFGGQTKVEIK 107
Db 61 RFGSGSGDTYLTITSSLPDDFATYFCQQGNTLPWTFGGQTKVEIK 107

RESULT 12

US-08-652-558-2
; Sequence 2, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-2

Query Match 84.5%; Score 480; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.5e-40;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSSLQPEDIATYFCHQYSKLPWTFGQGTKEIK 106
Db 61 RFGSGSGTDYTLTISSSLQPEDIATYFCHQYSKLPWTFGQGTKEIK 106

RESULT 13

US-08-437-642B-17
; Sequence 17, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992

; QUERY MATCH 84.5%; Score 480; DB 3; Length 107;
; Best Local Similarity 86.0%; Pred. No. 2.5e-40;
; Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESCA, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

US-08-437-642B-17

QY 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSSLQPEDIATYFCHQYSKLPWTFGQGTKEIK 107
Db 61 RFGSGSGTDYTLTISSSLQPEDIATYFCHQYSKLPWTFGQGTKEIK 107

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US-08-146-206C-17
; Sequence 17, Application US/08146206C
; Patent No. 6407213

; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-17

Query Match 84.5%; Score 480; DB 4; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.5e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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QY 61 RFGSGSGTDYTLTISSSLQPEDIATYFCHQYSKLPWTFGQGTKEIK 107
Db 61 RFGSGSGTDYTLTISSSLQPEDIATYFCHQYSKLPWTFGQGTKEIK 107

RESULT 15

US-09-705-686-17
; Sequence 17, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESCA, Leonard G.

; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/705,686
 ; FILING DATE: 02-No. 6639055-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/146206
 ; FILING DATE: 17-NOV-1993
 ; APPLICATION NUMBER: 07/715272
 ; FILING DATE: 14-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0709P1D3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-705-686-17

Query Match 84.5%; Score 480; DB 4; Length 107;
 Best Local Similarity 86.0%; Pred. No. 2.5e-40;
 Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
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 Qy 61 RFGSGSGTDYTLTITSSLPEDPATYFCHQYSKLPMTFGQGTKVEIK 107
 Db 61 RFGSGSGTDYTLTITSSLPEDPATYFCHQYSKLPMTFGQGTKVEIK 107

Search completed: August 1, 2005, 09:20:53
 Job time : 9.19913 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 28.4953 Seconds
(without alignments)
1476.651 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

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- 20: /cgn2_6/ptodata/2/pubpaa/US11 NEW PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	514	90.5	128	14	US-10-265-713-19
5	514	90.5	128	14	US-10-166-626-10
6	514	90.5	128	14	US-10-166-626-19
7	507	89.3	110	9	US-09-056-1608-103
8	507	89.3	110	14	US-10-234-671-101
9	507	89.3	110	17	US-10-974-591-101
10	507	89.3	237	9	US-09-056-1608-100
11	507	89.3	237	14	US-10-234-671-100
12	507	89.3	237	17	US-10-974-591-100
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14	507	88.9	107	9	US-09-056-1608-15
15	505	88.9	107	14	US-10-234-671-15
16	505	88.9	107	17	US-10-974-591-15
17	504	88.7	110	9	US-09-056-1608-105
18	504	88.7	110	14	US-10-234-671-103
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20	503	88.6	108	9	US-09-056-1608-8
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22	503	88.6	108	13	US-10-153-159-16
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28	503	88.6	108	17	US-10-877-532-7
29	503	88.6	110	14	US-10-234-671-8
30	503	88.6	110	15	US-10-624-153-94
31	503	88.6	110	17	US-10-683-043-1
32	503	88.6	110	17	US-10-974-591-8
33	503	88.6	667	16	US-10-764-428-25
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35	501	88.2	107	14	US-10-234-671-13
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60	498	87.7	107	16	US-10-723-434-1
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62	497	87.5	108	9	US-09-056-1608-126
63	497	87.5	108	14	US-10-234-671-124
64	497	87.5	108	17	US-10-974-591-124
65	496	87.3	213	16	US-10-379-392-155
66	492	86.6	213	16	US-10-379-392-157
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69	487	85.7	127	14	US-10-084-139-6
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Sequence 115, App
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Sequence 4, Appli
Sequence 6, Appli

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91 481 84.7 110 9 US-09-056-1608-115
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ALIGNMENTS

RESULT 1
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cdna KM-641

US-09-764-304-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; EARLIER FILING DATE: 2002-10-08
; EARLIER APPLICATION NUMBER: US/09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cdna KM-641

Query Match 90.5%; Score 514; DB 9; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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DB 21 DIQMTQTASSLPASLGRVTITCSASQDISNYLNWYQOKPKDGTGVKLLIFYSSNLSHGVPS 80
QY 61 RFSGGSGDTYLTITSSLPEDTIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 81 RFSGGSGDTYSLTISNLEPEDTIATYFCHQYSKLPWTFGGKLEIKR 128

RESULT 2
US-09-764-304-19
; Sequence 19, Application US/09764304

Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 90.5%; Score 514; DB 9; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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RESULT 3
US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA

US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; EARLIER FILING DATE: 2002-10-08
; EARLIER APPLICATION NUMBER: US/09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18

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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-265-713-10

Query Match          90.5%; Score 514; DB 14; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37;
Matches 96; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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QY 61 RPSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGGKTVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RPSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGKTVEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US/07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-265-713-19

Query Match          90.5%; Score 514; DB 14; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37;
Matches 96; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60
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Db 21 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPKDGTGTVKLLIFYSSNLHSGVPS 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RPSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGGKTVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RPSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGKTVEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US/07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-166-626-10

Query Match          90.5%; Score 514; DB 14; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37;
Matches 96; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPKDGTGTVKLLIFYSSNLHSGVPS 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RPSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGGKTVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RPSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGKTVEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US/07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: variable region
US-10-265-713-19

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RESULT 9

US-10-974-591-101
 ; Sequence 101, Application US/10974591
 ; Publication No. US20050112126A1
 ; GENERAL INFORMATION:

APPLICANT: Baca, Manuel
 ; Wells, James A.
 ; Presta, Leonard G.
 ; Lowman, Henry B.
 ; Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/974,591

FILING DATE: 26-Oct-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/723752

FILING DATE: 27-Nov-2000

APPLICATION NUMBER: 08/908469

FILING DATE: 06-Aug-1997

APPLICATION NUMBER: 08/833504

FILING DATE: 07-Apr-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-974-591-101

Query Match 89.3%; Score 507; DB 17; Length 110;

Best Local Similarity 88.0%; Pred. No. 2.4e-36;

Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60

Db 1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60

QY 61 RFGSGSGSDYTLTITSSLOPEDIATVFCQYSKLPMTFGQGTKEIKR 108

Db 61 RFGSGSGSDYTLTITSSLOPEDIATVFCQYSKLPMTFGQGTKEIKR 108

RESULT 10

US-09-056-1608-100

; Sequence 100, Application US/090561608

; Patent No. US20020032315A1

; GENERAL INFORMATION:

APPLICANT: Baca, Manuel

; Wells, James A.

; Applicant: Presta, Leonard G.

; Applicant: Lowman, Henry B.

APPLICANT: Chen, Yvonne M.
 ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
 ; NUMBER OF SEQUENCES: 131
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,1608

FILING DATE: 06-Apr-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856

FILING DATE: 06-Aug-1997

ATTORNEY/AGENT INFORMATION:

NAME: Haak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 237 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-056-1608-100

Query Match 89.3%; Score 507; DB 9; Length 237;

Best Local Similarity 88.0%; Pred. No. 5.2e-36;

Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60

Db 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 83

QY 61 RFGSGSGSDYTLTITSSLOPEDIATVFCQYSKLPMTFGQGTKEIKR 108

Db 84 RFGSGSGSDYTLTITSSLOPEDIATVFCQYSKLPMTFGQGTKEIKR 131

RESULT 11

US-10-234-671-100

; Sequence 100, Application US/10234671

; Publication No. US20030190317A1

; GENERAL INFORMATION:

APPLICANT: Baca, Manuel

; Wells, James A.

; Presta, Leonard G.

; Lowman, Henry B.

; Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-234-671-100

Query Match      89.3%; Score 507; DB 14; Length 237;
Best Local Similarity 88.0%; Pred. No. 5.2e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSNLSHGVPVS 60
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAPKLLIYFTSSLHSGVPVS 83

QY 61 RFSGGSGTDTLTLTSSLPEDFIATYFCHOYSKLPWTFGQGTKEIKR 108
Db 84 RFSGGSGTDTLTLTSSLPEDFIATYFCHOYSKLPWTFGQGTKEIKR 131

RESULT 12
US-10-974-591-100
; Sequence 100, Application US/10974591
; Publication No. US2005012126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
;

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-234-671-100

Query Match      89.3%; Score 507; DB 14; Length 237;
Best Local Similarity 88.0%; Pred. No. 5.2e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSNLSHGVPVS 60
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAPKLLIYFTSSLHSGVPVS 83

QY 61 RFSGGSGTDTLTLTSSLPEDFIATYFCHOYSKLPWTFGQGTKEIKR 108
Db 84 RFSGGSGTDTLTLTSSLPEDFIATYFCHOYSKLPWTFGQGTKEIKR 131

RESULT 13
US-10-011-125-2
; Sequence 2, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-2

Query Match      89.3%; Score 507; DB 13; Length 491;
Best Local Similarity 88.0%; Pred. No. 1.1e-35;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSNLSHGVPVS 60
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAPKLLIYFTSSLHSGVPVS 83

QY 61 RFSGGSGTDTLTLTSSLPEDFIATYFCHOYSKLPWTFGQGTKEIKR 108
Db 84 RFSGGSGTDTLTLTSSLPEDFIATYFCHOYSKLPWTFGQGTKEIKR 131

RESULT 14
US-09-056-160B-15
; Sequence 15, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
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; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-APR-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-056-160B-15

Query Match      88.9%; Score 505; DB 9; Length 107;
Best Local Similarity 88.8%; Pred. No. 3.5e-36;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTSPSSLASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYSKLPWTFGGTKVEIK 107
Db 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYSKLPWTFGGTKVEIK 107

RESULT 15
US-10-234-671-15
; Sequence 15, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-234-671-15

Query Match      88.9%; Score 505; DB 14; Length 107;
Best Local Similarity 88.8%; Pred. No. 3.5e-36;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTSPSSLASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYSKLPWTFGGTKVEIK 107
Db 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYSKLPWTFGGTKVEIK 107

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Job time : 28.4953 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.11574 Seconds
(without alignments)
1699.125 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

Sequence: 1 DIQMTQSPSLASVGRVT.....HOYSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	84.5	108	1 K1HUAV	Ig kappa chain V-I
2	479	84.3	111	2 A38740	Ig kappa chain V r
3	477	84.0	111	2 E38740	Ig kappa chain V r
4	472	83.1	111	2 C38740	Ig kappa chain V r
5	469	82.6	111	2 C38740	Ig kappa chain V r
6	466	82.0	107	2 B49026	Ig kappa chain V r
7	462	81.3	127	2 S40367	Ig kappa chain V-J
8	461	81.2	108	1 KVM573	Ig kappa chain V r
9	461	81.2	108	2 S69900	Ig kappa chain (cl)
10	456	80.3	108	1 K1HURE	Ig kappa chain V-I
11	454	79.9	122	2 A29380	Ig kappa chain pre
12	452	79.6	108	2 S69303	Ig kappa chain (cl)
13	452	79.6	115	2 JL0080	Ig kappa chain pre
14	451	79.4	129	2 S52789	Ig kappa chain V r
15	450	79.2	110	2 S44118	Ig kappa chain V-J
16	448	78.9	108	1 KVM5AR	Ig kappa chain V r
17	447	78.7	108	2 S69902	Ig kappa chain (cl)
18	447	78.7	109	2 PH0888	Ig kappa chain V r
19	447	78.7	126	2 A34904	Ig kappa chain pre
20	445	78.3	108	1 K1HUNG	Ig kappa chain V-I
21	445	78.3	108	2 I39154	Ig kappa chain (BR)
22	445	78.3	125	2 S40333	Ig kappa chain V-J
23	444	78.2	128	2 A26406	Ig kappa chain V r
24	443.5	78.1	107	2 S69901	Ig kappa chain (cl)
25	443	78.0	139	2 S40365	Ig kappa chain - h
26	442	77.8	123	2 S40331	Ig kappa chain - h
27	442	77.8	131	2 S40352	Ig kappa chain V-J
28	441.5	77.7	108	2 S38862	Ig kappa chain V r
29	441	77.6	108	2 B49047	Ig kappa chain V r

30	440	77.5	107	2 A48677	Ig kappa chain V-J
31	439	77.3	108	2 S44122	Ig kappa chain V r
32	439	77.3	108	2 C26405	Ig kappa chain V r
33	438	77.1	108	1 K1HURY	Ig kappa chain V-I
34	438	77.1	108	2 S19570	Ig kappa chain V r
35	437.5	77.0	107	2 S36275	Ig lambda chain V
36	437	76.9	107	2 B48677	Ig kappa chain V-J
37	437	76.9	107	2 B28044	Ig kappa chain V r
38	436	76.8	108	2 PL0282	Ig kappa chain V r
39	435	76.6	109	2 S31998	Ig kappa chain - h
40	434	76.4	107	2 S36264	Ig lambda chain V
41	434	76.4	107	2 A28044	Ig kappa chain V r
42	433	76.2	107	2 D48677	Ig kappa chain V-J
43	433	76.2	108	1 K1HUME	Ig kappa chain V-I
44	433	76.2	108	2 B26405	Ig kappa chain V r
45	433	76.2	127	2 PH1224	Ig kappa chain pre
46	431	75.9	129	2 S40369	Ig kappa chain - h
47	430.5	75.8	107	2 S69906	Ig kappa chain (cl)
48	429	75.5	108	1 K1HULY	Ig kappa chain V-I
49	429	75.5	108	2 S19674	Ig kappa chain V r
50	429	75.5	109	2 S31981	Ig kappa chain - h
51	429	75.5	141	2 A49134	Ig kappa chain V-I
52	427	75.2	107	2 S32188	Ig kappa chain V r
53	426.5	75.1	124	2 S40336	Ig kappa chain V-J
54	425	74.8	105	2 PH0087	Ig kappa chain V r
55	425	74.8	135	2 S24320	Ig kappa chain pre
56	424	74.6	107	2 I69017	Ig kappa chain V-I
57	424	74.6	108	1 K1HUHU	Ig kappa chain V-I
58	423.5	74.6	106	2 PC2397	anti-tetanus toxin
59	423	74.5	108	2 B30551	Ig kappa chain V r
60	423	74.5	108	2 S11124	Ig kappa chain V r
61	422	74.3	126	2 S40335	Ig kappa chain V-J
62	422	74.3	129	1 K1HUMK	Ig kappa chain pre
63	421	74.1	107	2 C48677	Ig light chain V-J
64	421	74.1	117	2 S46371	Ig kappa chain V-J
65	420	73.9	107	2 JL0139	Ig kappa chain V r
66	420	73.9	108	1 K1HUKA	Ig kappa chain V-I
67	420	73.9	108	1 K1HUSW	Ig kappa chain V-I
68	420	73.9	125	2 S40349	Ig kappa chain V-J
69	419.5	73.9	125	2 S40315	Ig kappa chain - h
70	419	73.8	108	1 K1HUBN	Ig kappa chain V-I
71	419	73.8	122	2 S40370	Ig kappa chain - h
72	419	73.8	129	2 S52793	Ig kappa chain V r
73	419	73.8	132	2 S40334	Ig kappa chain - h
74	418	73.6	108	1 K1HUKU	Ig kappa chain V-I
75	418	73.6	108	2 S47182	Ig kappa chain - h
76	418	73.6	117	2 S46376	Ig kappa chain V-J
77	418	73.6	117	2 S42263	Ig kappa chain V r
78	418	73.6	117	2 S43528	Ig kappa chain V r
79	418	73.6	122	2 S40314	Ig kappa chain - h
80	417	73.4	108	1 K1HUBI	Ig kappa chain V-I
81	417	73.4	129	2 S40317	Ig kappa chain - h
82	416	73.2	108	1 K1HOUU	Ig kappa chain V-I
83	416	73.2	120	2 S46370	Ig kappa chain V-J
84	416	73.2	129	2 S52792	Ig kappa chain V r
85	416	73.2	130	2 S40368	Ig kappa chain - h
86	415	73.1	107	2 S36262	Ig lambda chain V
87	415	73.1	128	2 S46372	Ig light chain var
88	414	72.9	107	2 S36269	Ig lambda chain V
89	414	72.9	109	2 S31979	Ig kappa chain - h
90	413	72.7	108	1 K1HUSW	Ig kappa chain V-I
91	413	72.7	124	2 S40318	Ig kappa chain V r
92	412	72.5	95	2 PH0862	Ig kappa chain V r
93	412	72.5	108	1 K1HUGL	Ig kappa chain V-I
94	411	72.4	95	2 PH0864	Ig kappa chain V r
95	411	72.4	108	1 K1HUDE	Ig kappa chain V-I
96	411	72.4	125	2 S40316	Ig kappa chain - h
97	410	72.2	109	2 S31980	Ig kappa chain - h
98	410	72.2	109	2 S31978	Ig kappa chain - h
99	410	72.2	124	2 S40348	Ig kappa chain V-J
100	410	72.2	132	2 S38646	Ig kappa chain V r

ALIGNMENTS

RESULT 1

KIHUAV
Ig kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: A91653; A01863; S02573
R:Schiebel, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653
A:Molecule type: protein
A:Residues: 1-108 <SCH>
A:Cross-references: UNIPROT:P01594
A:Note: the C region of this chain has the Inv (3) marker
R:Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A:Title: The structure determination of the variable portion of the Bence-Jones protein
A:Reference number: A30729; MUID:77022433; PMID:1234024
A:Contents: annotation; X-ray crystallography
A:Note: the structure of the V region was determined by molecular replacement methods us
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
A:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 84.5%; Score 480; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 1.7e-36;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
QY 61 RFSGGSGTDYTLTISSLOPEDVIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGGAHFTTISLQPEDVIATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 2

A38740
Ig kappa chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: A38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 479; DB 2; Length 111;
Best Local Similarity 80.6%; Pred. No. 2.2e-36;
Matches 87; Conservative 14; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
DB 4 DVQMTQTTSLSASLGDRVTITCSASQGISNYLNWYQOKPDGTVKLLIYVTSLSLHSGVPS 63
QY 61 RFSGGSGTDYTLTISSLOPEDVIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 64 RFSGGSGTDYSLTISNLEPEDVIATYFCHQYSKLPWTFGGQGTKEIKR 111

RESULT 3

E38740
Ig kappa chain V region (Py54) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: E38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: E38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 477; DB 2; Length 111;
Best Local Similarity 81.5%; Pred. No. 3.3e-36;
Matches 88; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
DB 4 DVMTQTTSLSASLGDRVTITCSASQGISNYLNWYQOKPDGTVKLLIYVTSLSLHSGVPS 63
QY 61 RFSGGSGTDYTLTISSLOPEDVIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 64 RFSGGSGTDYSLTISDLEPEDVIATYFCHQYSKLPWTFGGQGTKEIKR 111

RESULT 4

G38740
Ig kappa chain V region (Py69) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: G38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: G38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 472; DB 2; Length 111;
Best Local Similarity 81.5%; Pred. No. 9.4e-36;
Matches 88; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
DB 4 DVLMTQSTSSLSASLGDRVTITCSASQDISNYLNWYQOKPDGTVKLLIYVTSLSLHSGVPS 63
QY 61 RFSGGSGTDYTLTISSLOPEDVIATYFCHQYSKLPWTFGQGTKEIKR 108

Qy	61	RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPTWTFGQTKVEIKR	108
		: : : : : :	
Db	61	RFSGGSGTDYSLTISBLZP2BATATYCCOYSKLPRTFGGTGLEIKR	108

```
RESULT 9
S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69900; S69907; S69908
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69900
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55041; NID:G511023; PIDN:CAA38881.1; PID:G511024
A:Accession: S69907
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY2>
A:Cross-references: EMBL:X55048; NID:G511037; PIDN:CAA38888.1; PID:G511038
A:Accession: S69908
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY3>
A:Cross-references: EMBL:X55049; NID:G511039; PIDN:CAA38889.1; PID:G511040
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 461; DB 2; Length 108;
Best Local Similarity 80.6%; Pred. No. 9e-35; Indels 0; Gaps 0;
Matches 87; Conservative 10; Mismatches 11;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQKPKDGTGKLLIYTSRLSHGVPVS 60

QY 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGQGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGKTKLEIKR 108

RESULT 10
KLHURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A91663; A01873
R:Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A:Title: Die Primärstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom K
vollständige Aminosäuresequenz des Proteins.
A:Reference number: A91663; MUID:76023758; PMID:809329
A:Accession: A91663
A:Molecule type: Protein
A:Residues: 1-108 <PAL>
A:Cross-references: UNIPROT:P01607
A:Note: The C region of this chain has the Inv (1,2) marker
R:Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A:Title: The molecular structure of a dimer composed of the variable portions of the Ben
A:Reference number: A90393; MUID:7603968; PMID:1182131
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
```

```
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status experimental

Query Match      80.3%; Score 456; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 2.5e-34;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDIILKLNWYQQTGKAPKLLIYTSNLSHGVPVS 60

QY 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGQGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGKTKLEIKR 108

RESULT 11
A29380
Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C:Accession: A29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable ;
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match      79.9%; Score 454; DB 2; Length 122;
Best Local Similarity 79.6%; Pred. No. 4.3e-34;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 15 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQKPKDGTGKLLIYTSRLSHGVPVS 74

QY 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGQGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 75 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGKTKLEIKR 122

RESULT 12
S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69903; S69904; S69905
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69903
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55044; NID:G511029; PIDN:CAA38884.1; PID:G511030
A:Accession: S69904
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY2>
A:Cross-references: EMBL:X55045; NID:G511031; PIDN:CAA38885.1; PID:G511032
A:Accession: S69905
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY3>
A:Cross-references: EMBL:X55046; NID:G511033; PIDN:CAA38886.1; PID:G511034
```


DESC LOCAL SIMILARITY 01.3%; FREQ. NO. 0.00E-34;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 28.0249 Seconds
(without alignments)
1973.408 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

Sequence: 1 DIQMTQSPSLSSASVGRVT.....HOYSKLPWTFGGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	480	84.5	108	1	P01594 homo sapien
2	461	81.2	108	1	KV1B_HUMAN
3	456	80.3	108	1	KV5J_MOUSE
4	448	78.9	108	1	KV10_HUMAN
5	447	78.7	108	1	KV5K_MOUSE
6	447	78.7	108	1	KV5L_MOUSE
7	445	78.3	108	1	KV5M_MOUSE
8	445	78.3	108	1	KV1A_HUMAN
9	445	78.3	108	2	KV5O_MOUSE
10	443	78.0	108	1	KV5N_MOUSE
11	439	77.3	236	2	Q6GMW1
12	438	77.1	108	1	KV1P_HUMAN
13	436	76.8	108	1	KV1Y_HUMAN
14	434	76.4	108	2	Q9UL70
15	433.5	76.3	107	2	Q96SA9
16	433	76.2	108	1	KV1R_HUMAN
17	433	76.2	236	2	Q6GMX9
18	430	75.7	108	1	KV5U_MOUSE
19	430	75.7	236	2	Q723Y4
20	429	75.5	107	2	Q9JL84
21	429	75.5	108	1	KV1M_HUMAN
22	427	75.2	236	2	Q6GMX8
23	424	74.6	108	1	KV1H_HUMAN
24	423	74.5	236	2	Q6GMX0
25	422	74.3	129	1	KV1W_HUMAN
26	420	73.9	108	1	KV1K_HUMAN
27	420	73.9	108	1	KV1Q_HUMAN
28	419	73.8	108	1	KV1V_HUMAN
29	418	73.6	108	1	KV1L_HUMAN
30	417	73.4	108	1	KV1C_HUMAN
31	416.5	73.3	107	2	Q9UL81

ALIGNMENTS

32	416	73.2	108	1	KVIN_HUMAN	P01606 homo sapien
33	416	73.2	116	2	Q96PF6	Q96PF6 homo sapien
34	414	72.9	236	2	Q6PIH7	Q6PIH7 homo sapien
35	413	72.7	108	1	KV1S_HUMAN	P01611 homo sapien
36	413	72.7	244	2	Q65ZC8	Q65ZC8 homo sapien
37	412	72.5	108	1	KV1G_HUMAN	P01599 homo sapien
38	411	72.4	108	1	KV1E_HUMAN	P01597 homo sapien
39	411	72.4	234	2	Q72473	Q72473 homo sapien
40	408.5	71.9	107	1	KVID_HUMAN	P01596 homo sapien
41	408	71.8	240	2	Q65ZC9	Q65ZC9 homo sapien
42	405.5	71.4	109	1	KV1T_HUMAN	P01612 homo sapien
43	403	71.0	108	2	Q9UL79	Q9UL79 homo sapien
44	400	70.4	108	1	KV1P_HUMAN	P01598 homo sapien
45	394	69.4	236	2	Q6PIH4	Q6PIH4 homo sapien
46	394	69.4	236	2	Q6PII5	Q6PII5 homo sapien
47	393	69.2	134	1	KV4C_HUMAN	P06314 homo sapien
48	388	68.3	108	1	KV5S_MOUSE	P01652 mus musculus
49	388	68.3	129	1	KV1X_HUMAN	P04432 homo sapien
50	384	67.6	130	1	KV5G_MOUSE	P01639 mus musculus
51	379	66.7	108	1	KV5Q_MOUSE	P01650 mus musculus
52	379	66.7	117	1	KV1I_HUMAN	P01601 homo sapien
53	376	66.2	236	2	Q7TS98	Q7TS98 mus musculus
54	374	65.8	108	1	KV5P_MOUSE	P01649 mus musculus
55	373	65.7	108	1	KV5T_MOUSE	P01653 mus musculus
56	373	65.7	109	2	Q920E6	Q920E6 mus musculus
57	373	65.7	112	1	KV1U_HUMAN	P01613 homo sapien
58	371	65.3	114	1	KV4A_HUMAN	P01625 homo sapien
59	371	65.3	117	1	KV1J_HUMAN	P01602 homo sapien
60	368	64.8	108	1	KV5R_MOUSE	P01651 mus musculus
61	365	64.3	128	1	KV5E_MOUSE	P01637 mus musculus
62	362.5	63.8	129	1	KV3M_HUMAN	P18136 homo sapien
63	362.5	63.8	133	1	KV4B_HUMAN	P06313 homo sapien
64	360.5	63.5	243	2	Q7TQM2	Q7TQM2 mus musculus
65	359	63.2	127	2	Q925S9	Q925S9 mus musculus
66	357.5	62.9	110	1	KV3P_MOUSE	P01668 mus musculus
67	357	62.9	298	2	Q9QVFO	Q9QVFO synthetic c
68	356	62.7	111	1	KV3O_MOUSE	P01667 mus musculus
69	356	62.7	111	1	KV3Q_MOUSE	P01669 mus musculus
70	355.5	62.6	109	1	KV3D_HUMAN	P01622 homo sapien
71	355.5	62.6	134	2	Q8VDD0	Q8VDD0 mus musculus
72	353.5	62.2	109	1	KV3B_HUMAN	P01620 homo sapien
73	353.5	62.2	109	1	KV3E_HUMAN	P01623 homo sapien
74	353.5	62.2	129	1	KV3H_HUMAN	P04207 homo sapien
75	353.5	62.2	129	1	KV3L_HUMAN	P18135 homo sapien
76	353	62.1	238	2	Q6GJS7	Q6GJS7 mus musculus
77	352	62.0	108	2	Q8VIJ0	Q8VIJ0 mus musculus
78	351	61.8	108	1	KV5D_MOUSE	P01636 mus musculus
79	350.5	61.7	109	1	KV3F_HUMAN	P01624 homo sapien
80	350.5	61.7	112	2	Q8K1F3	Q8K1F3 mus musculus
81	349	61.4	136	1	KV5B_MOUSE	P01634 mus musculus
82	347.5	61.2	109	2	Q9UL78	Q9UL78 homo sapien
83	347	61.1	149	1	KV5A_MOUSE	P01633 mus musculus
84	346	60.9	108	2	Q9UL83	Q9UL83 homo sapien
85	346	60.9	111	1	KV3M_MOUSE	P01665 mus musculus
86	345.5	60.8	114	2	Q8K1F1	Q8K1F1 mus musculus
87	345.5	60.8	235	2	Q6GMW0	Q6GMW0 homo sapien
88	345	60.7	112	1	KV3G_MOUSE	P01659 mus musculus
89	343	60.4	132	1	KV3F_MOUSE	P01658 mus musculus
90	342.5	60.3	112	2	Q8K1F2	Q8K1F2 mus musculus
91	342	60.2	111	1	KV3L_MOUSE	P01664 mus musculus
92	342	60.2	111	2	Q920E9	Q920E9 mus musculus
93	340	59.9	111	1	KV3N_MOUSE	P01666 mus musculus
94	339.5	59.8	235	2	Q6PJF2	Q6PJF2 homo sapien
95	339	59.7	111	1	KV3A_MOUSE	P01654 mus musculus
96	338	59.5	109	1	KV4D_HUMAN	P83593 homo sapien
97	338	59.5	262	2	Q65Z11	Q65Z11 mus musculus
98	337	59.3	111	1	KV3R_MOUSE	P01670 mus musculus
99	337	59.3	111	1	KV3S_MOUSE	P01671 mus musculus
100	337	59.3	131	1	KV3I_MOUSE	P01661 mus musculus

21-JUL-1986 (Rel. 01, Last sequence update)
 25-OCT-2004 (Rel. 45, Last annotation update)
 Ig kappa chain V-I region Rel.1.
 Homo sapiens (Human).
 Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE.
 MEDLINE=76023758; PubMed=809329;
 Palm W., Hilechmann N.;
 "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 and characterization of the tryptic peptides; the complete amino acid
 sequence of the protein; a contribution to the elucidation of the
 three-dimensional structure of antibodies, in particular their
 combining site.";
 Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).
 [2]
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 MEDLINE=76039968; PubMed=1182131;
 RA Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.;
 "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein REI refined at 2.0-A resolution.";
 Biochemistry 14:4943-4952 (1975).
 CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 marker.
 CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91663; KIHURE.
 DR PDB; 1AR2; X-ray; @=1-107.
 DR PDB; 1BWW; X-ray; A/B=1-107.
 DR PDB; 1RBI; X-ray; A/B=1-107.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT STRAND 60 61
 FT TURN 62 67
 FT STRAND 68 69
 FT TURN 70 75
 FT STRAND 80 82
 FT STRAND 84 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;
 Query Match 80.3%; Score 456; DB 1; Length 108;

Best Local Similarity 80.6%; Pred. No. 3.2e-40;
 Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQOKPKAVKLLIFVSSNLHSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQOKPKAVKLLIFVSSNLHSGVPS 60
 QY 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
 DB 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
 RESULT 4
 KV5K MOUSE
 ID KV5K MOUSE STANDARD; PRT; 108 AA.
 AC P01644;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region HP R16.7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype.";
 Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
 CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR PIR; A01927; KMSAR.
 DR HSSP; P01594; LJV5.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 108 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11910 MW; A554642C63BFF597 CRC64;
 Query Match 78.9%; Score 448; DB 1; Length 108;
 Best Local Similarity 79.6%; Pred. No. 2.2e-39;
 Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQOKPKAVKLLIFVSSNLHSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQOKPKAVKLLIFVSSNLHSGVPS 60
 QY 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
 DB 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
 RESULT 5
 KV5L MOUSE
 ID KV5L MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)

```
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE.
RP STRAIN=A/J;
RC MEDLINE=82150934; PubMed=6801658;
RX Siegelman M., Capra J.D.;
RA "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01607; IRII.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Complementarity-determining-4.
FT DOMAIN 89 97 By similarity.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFPF58E CRC64;

Query Match 78.7%; Score 447; DB 1; Length 108;
Best Local Similarity 79.6%; Pred. No. 2.9e-39;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKAVKLLIFYSNLHSGVPS 60
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYTSRLHSGVPS 60

OY 61 RFSGGSGTDYLTITSSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDYSLTISNLEQEDIATYFCQGGVMLPRTEGGGKLEIKR 108

RESULT 6
KV5M_MOUSE
ID KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE.
RP STRAIN=A/J;
RC MEDLINE=82150934; PubMed=6801658;
RX Siegelman M., Capra J.D.;
RA "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JUV5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.

Query Match 78.7%; Score 447; DB 1; Length 108;
Best Local Similarity 79.6%; Pred. No. 2.9e-39;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKAVKLLIFYSNLHSGVPS 60
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYTSRLHSGVPS 60

OY 61 RFSGGSGTDYLTITSSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDYSLTISNLEQEDIATYFCQGGVMLPRTEGGGKLEIKR 108

RESULT 7
KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RP MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Complementarity-determining-4.
FT DOMAIN 89 97 By similarity.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 78.3%; Score 445; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 4.7e-39;
Matches 85; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
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DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Complementarity-determining-4.
FT DOMAIN 89 97 By similarity.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 78.7%; Score 447; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 2.9e-39;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPKAVKLLIFYSNLHSGVPS 60
DB 1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYTSRLHSGVPS 60

OY 61 RFSGGSGTDYLTITSSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDYSLTISNLEQEDIATYFCQGGVMLPRTEGGGKLEIKR 108

RESULT 7
KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RP MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Complementarity-determining-4.
FT DOMAIN 89 97 By similarity.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 78.3%; Score 445; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 4.7e-39;
Matches 85; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
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Qy 1 DIQMTSPSSLSASVGRVITTCASQDISNLYNWYQKPKAVKLLIFYSNHLHSGVPS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTSPSSLSASVGRVITTCASQDISNLYNWYQKPKAVKLLIFYSNHLHSGVPS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFSGSGSDTYLTITISLQPEDIATYFCHQYKLPWTFGGTKVEIKR 108
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSDTYLTITISLQPEDIATYFCHQYKLPWTFGGTKVEIKR 108
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
KV50 MOUSE
ID_KV50_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 78.3%; Score 445; DB 1; Length 108;
Best Local Similarity 77.8%; Pred. No. 4.7e-39;
Matches 84; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGRVITTCASQDISNLYNWYQKPKAVKLLIFYSNHLHSGVPS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTSPSSLSASVGRVITTCASQDISNLYNWYQKPKAVKLLIFYSNHLHSGVPS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFSGSGSDTYLTITISLQPEDIATYFCHQYKLPWTFGGTKVEIKR 108
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSDTYLTITISLQPEDIATYFCHQYKLPWTFGGTKVEIKR 108
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR HSSP; P01607; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 78.3%; Score 445; DB 2; Length 108;
Best Local Similarity 79.6%; Pred. No. 4.7e-39;
Matches 86; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGRVITTCASQDISNLYNWYQKPKAVKLLIFYSNHLHSGVPS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTSPSSLSASVGRVITTCASQDISNLYNWYQKPKAVKLLIFYSNHLHSGVPS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFSGSGSDTYLTITISLQPEDIATYFCHQYKLPWTFGGTKVEIKR 108
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSDTYLTITISLQPEDIATYFCHQYKLPWTFGGTKVEIKR 108
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
KV5N MOUSE
ID_KV5N_MOUSE STANDARD; PRT; 108 AA.
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01607; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
```

```
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EF2A2 CRC64;

Query Match 77.3%; Score 439; DB 2; Length 236;
Best Local Similarity 81.3%; Pred. No. 5.1e-38;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLHSGVPSR 61
DB 24 IQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLHSGVPSR 83

QY 62 FSGSGSGTDYTLTISSLQPEDIAFYCHQYKLPWTFQGTGKVEIKR 108
DB 84 FSGSGSGTDYTLTISSLQPEDIAFYCHQYKLPWTFQGTGKVEIKR 130

RESULT 12
KVLP_HUMAN STANDARD; PRT; 108 AA.
ID KVLP_HUMAN
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
Cum.)";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.;
RA (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
York (1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 77.1%; Score 438; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 2.5e-38;
Matches 85; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLHSGVPS 60

QY 61 FSGSGSGTDYTLTISSLQPEDIAFYCHQYKLPWTFQGTGKVEIKR 108
DB 61 FSGSGSGTDYTLTISSLQPEDIAFYCHQYKLPWTFQGTGKVEIKR 108

RESULT 11
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusik A., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszynski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6EA087AFAC437 CRC64;
```



```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 76.3%; Score 433.5; DB 2; Length 107;
Best Local Similarity 81.7%; Pred.No. 7.5e-38;
Matches 89; Conservative 6; Mismatches 11; Indels 3; Gaps 2;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQISIVYLNWYQKPKAVKLLIFYSNLSHGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISIVYLNWYQKPKAVKLLIFYSNLSHGVPS 60

QY 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQSYSTL--TFGGGTKVEIKR 108
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQSYSTL--TFGGGTKVEIKR 107

```

Search completed: August 1, 2005, 09:17:09
 Job time : 28.0249 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 35.8407 Seconds
(without alignments)
1284.140 Million cell updates/sec

Title: US-10-089-500-55
Perfect score: 624
Sequence: 1 EVTLVSGGDFVRPGGSLKV.....KLCTYYFDSMGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003s:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	119	4	AAB81989
2	624	100.0	119	6	ABU11012
3	624	100.0	130	2	AAR33256
4	624	100.0	130	2	AAR53341
5	624	100.0	130	2	AAY28369
6	624	100.0	130	3	AAB01627
7	624	100.0	138	4	AAB81977
8	624	100.0	138	6	ABU11002
9	624	100.0	582	4	AAB81991
10	579	92.8	119	4	AAB81985
11	579	92.8	119	6	ABU11010
12	579	92.8	582	4	AAB81987
13	493	79.0	119	2	AAB29994
14	487	78.0	134	6	ABP60555
15	486.5	78.0	294	4	AAB20442
16	486.5	78.0	325	4	AAB20438
17	486.5	78.0	732	4	AAB20437
18	486	77.9	140	6	ABG74241
19	486	77.9	247	2	AAW11917
20	482.5	77.3	249	4	AAB20436
21	481	77.1	121	5	AAE16426
22	480.5	77.0	121	6	ABR41818
23	480	76.9	119	2	AAB29996
24	480	76.9	237	7	AAE38657
25	477.5	76.5	121	8	ADM78071

XX PD 24-MAR-1993.
XX XX
XX PF 18-SEP-1992; 92EP-00116026.
XX XX
XX PR 18-SEP-1991; 91JP-00238375.
XX XX
XX PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX XX
XX PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX XX
XX DR WPI; 1993-095510/12.
XX DR N-PSDB; AAQ33257.
XX XX
XX PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
XX PT cancers, such as melanoma, neuroblastoma, etc.
XX XX
XX PS Claim 6; Page 29-30; 63pp; English.
XX XX
XX CC The sequences given in AAR33256-57 represent rat heavy and light chain
XX CC variable regions respectively. The DNA sequences encoding these proteins
XX CC were used in the construction of humanised chimeric antibody expression
XX CC vectors. In these humanised antibodies none of the amino acids of the non
XX CC -human animal Ab variable region have been changed. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX XX
XX SQ Sequence 130 AA;
Query Match 100.0%; Score 624; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.6e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVSACAAGFAFSGHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
DB 11 EVTLVESGGDFVKPGGSLKVSACAAGFAFSGHYAMSWVRQTPAKRLEWVAYISSGGSTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129
RESULT 4
AAR53341
ID AAR53341 standard; protein; 130 AA.
AC AAR53341;
XX XX
XX DT 18-NOV-1994 (first entry)
XX XX
XX DE KM641 L chain variable region.
XX XX
XX KW Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
XX KW expression vector; heavy; light; chain; hypervariable region; CDR;
XX KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX XX
XX OS Mus musculus.
XX XX
XX PH Key Location/Qualifiers
XX FT Peptide 1..10
XX FT /label= eig_peptide
XX XX
XX PN AU9346181-A.
XX XX
XX PD 17-MAR-1994.
XX XX
XX PF 07-SEP-1993; 93AU-00046181.
XX XX
XX PR 07-SEP-1992; 92JP-00238452.
XX XX
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX XX

DR WPI; 1994-126857/16.
DR N-PSDB; AAQ45439.
XX XX
XX PT Humanised antibody specific for ganglioside GM2 - used for producing a
XX PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX XX
XX PS Example 2; Page 116-117; 191pp; English.
XX XX
XX CC Example 2 describes the construction of the vector pCh1641HA1 for
XX CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
XX CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
XX CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
XX CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
XX CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
XX CC was constructed by joining the H chain variable region gene from
XX CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
XX CC synthetic DNAs given in AAQ63439 and AAQ63440
XX XX
XX SQ Sequence 130 AA;
Query Match 100.0%; Score 624; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.6e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVSACAAGFAFSGHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
DB 11 EVTLVESGGDFVKPGGSLKVSACAAGFAFSGHYAMSWVRQTPAKRLEWVAYISSGGSTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129
RESULT 5
AAY28369
ID AAY28369 standard; protein; 130 AA.
XX XX
XX AC AAY28369;
XX XX
XX DT 04-NOV-1999 (first entry)
XX XX
XX DE pKM641 HA3 immunoglobulin heavy chain.
XX XX
XX KW antibody; nucleotide; genomic; hypervariable region; chimeric;
XX KW light chain; amino acid.
XX XX
XX OS Mus sp.
XX XX
XX PN US5939532-A.
XX PD 17-AUG-1999.
XX XX
XX PF 07-JUN-1995; 95US-00483528.
XX XX
XX PR 07-SEP-1993; 93US-00116778.
XX XX
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX XX
XX DR WPI; 1999-468416/39.
XX DR N-PSDB; AAX99482.
XX XX
XX PT Chimeric human antibody expression vectors.
XX PS Example 1; Col 99-101; 188pp; English.
XX XX
XX CC This immunoglobulin region was isolated from pKM641HA3. This sequence has
XX CC no methionine initiation codon and the leader sequence was partly
XX CC lacking. The chimeric human antibodies are useful in the treatment of
XX CC cancer, especially that which is of neural ectodermal origin. In contrast
XX CC to prior art constructs based on mouse monoclonal antibodies, the
XX CC chimeric human antibodies do not cause anti-mouse immunoglobulin

ID ABU1002 standard; protein; 138 AA.
 AC ABU1002;
 XX
 DT 04-FEB-2003 (first entry)
 XX
 DE Modified ganglioside GD3 antibody associated protein #1.
 XX
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX
 OS Mus musculus.
 XX
 PN WO200278739-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-JP003170.
 XX
 PR 29-MAR-2001; 2001JP-00097483.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX
 XX WPI; 2003-067410/06.
 DR
 XX
 PT Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX
 XX Example 3; Page 97; 121pp; Japanese.
 XX
 CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 XX
 SQ Sequence 138 AA;
 Query Match 100.0%; Score 624; DB 6; Length 138;
 Best Local Similarity 100.0%; Pred. NO. 9.2e-51;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVTLVSGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
 DB 20 EVTLVSGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 79
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYYPDSMGQGTTLTVSS 119
 DB 80 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYYPDSMGQGTTLTVSS 138
 RESULT 9
 AAB81991
 ID AAB81991 standard; protein; 582 AA.
 AC AAB81991;
 XX
 DT 03-JUL-2001 (first entry)
 XX
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
 XX
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KW cancer.
 XX
 OS Synthetic.
 XX
 PN WO200123432-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-JP005774.
 XX
 PR 30-SEP-1999; 99JP-00278291.
 XX
 PR 06-APR-2000; 2000JP-00105088.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX
 XX WPI; 2001-266143/27.
 DR
 XX
 PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-JP006774.
 XX
 PR 30-SEP-1999; 99JP-00278291.
 XX
 PR 06-APR-2000; 2000JP-00105088.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX
 XX WPI; 2001-266143/27.
 DR
 XX
 PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT activity in cancer.
 XX
 XX Claim 39; Page 175-179; 183pp; Japanese.
 PS
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumours, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 SQ Sequence 582 AA;
 Query Match 100.0%; Score 624; DB 4; Length 582;
 Best Local Similarity 100.0%; Pred. NO. 4.4e-50;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVTLVSGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
 DB 1 EVTLVSGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYYPDSMGQGTTLTVSS 119
 DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYYPDSMGQGTTLTVSS 119
 RESULT 10
 AAB81985
 ID AAB81985 standard; protein; 119 AA.
 AC AAB81985;
 XX
 DT 03-JUL-2001 (first entry)
 XX
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.
 XX
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KW cancer.
 XX
 OS Synthetic.
 XX
 PN WO200123432-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-JP005774.
 XX
 PR 30-SEP-1999; 99JP-00278291.
 XX
 PR 06-APR-2000; 2000JP-00105088.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Hanai N, Shitara K, Nakamura K, Niwa R;
 XX
 XX WPI; 2001-266143/27.
 DR
 XX
 PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
PS Claim 20; Page 142-143; 183pp; Japanese.
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 119 AA;
SQ
Query Match 92.8%; Score 579; DB 4; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.3e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAF SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
RESULT 11
ABU11010
ID ABU11010 standard; protein; 119 AA.
XX
AC ABU11010;
XX
XX 04-FEB-2003 (first entry)
DT
XX Modified ganglioside GD3 antibody associated protein #3.
DE
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX Synthetic.
OS
XX WO200278739-A1.
PN
XX 10-OCT-2002.
PD
XX 29-MAR-2002; 2002WO-JP003170.
PF
XX 29-MAR-2001; 2001JP-00097483.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Shitara K, Niwa R, Kanazawa J, Asada M;
PI
XX WPI; 2003-067410/06.
DR
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
PT
XX
XX Claim 8; Page 99; 121pp; Japanese.
PS
XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 119 AA;
SQ
Query Match 92.8%; Score 579; DB 6; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.3e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAF SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
RESULT 12
AAB81987
ID AAB81987 standard; protein; 582 AA.
XX
AC AAB81987;
XX
XX 03-JUL-2001 (first entry)
DT
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
XX Synthetic.
OS
XX WO200123432-A1.
PN
XX 05-APR-2001.
PD
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
DR
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Claim 41; Page 168-172; 183pp; Japanese.
PS
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 582 AA;
SQ
Query Match 92.8%; Score 579; DB 4; Length 582;
Best Local Similarity 91.6%; Pred. No. 7.3e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAF SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
RESULT 13
AAW29994
ID AAW29994 standard; protein; 119 AA.
XX

AAW29994;
 25-MAR-2003 (revised)
 12-MAR-1998 (first entry)
 Heavy chain variable region of MAb ior t1A.
 Heavy chain; variable region; monoclonal antibody; human; CD6; murine;
 leukocyte differentiation antigen; hybridoma; humanisation; mutagenesis;
 PCR; primer; amplification; inflammatory infiltration; skin; psoriasis;
 diagnosis.
 Mus sp.
 WO9719111-A2.
 29-MAY-1997.
 18-NOV-1996; 96WO-CU000004.
 17-NOV-1995; 95CU-00000120.
 (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 Montero Casimiro JE, Lombardero Valladares J, Perez Rodriguez R;
 Sierra Blazquez P, Tormo Bravo BR;
 WPI; 1997-298060/27.
 Monoclonal antibody against human CD6 antigen - useful for diagnosis and
 treatment of psoriasis.
 Claim 3; Page 27; 38pp; Spanish.
 This is the amino acid sequence of the heavy chain variable region of the
 monoclonal antibody (MAb) ior t1A which recognises the human leukocyte
 differentiation antigen CD6. The MAb is a murine IgG2-type Ab produced by
 the usual hybridoma techniques. The coding sequence for the variable
 region can be used to generate humanised variants, especially by
 mutagenic PCR. CD6 has been shown to be expressed in T lymphocytes
 involved in the inflammatory infiltration of the skin in psoriasis. The
 anti-CD6 MAb can therefore be used to diagnose and treat psoriasis.
 (Updated on 25-MAR-2003 to correct PA field.)
 SQ Sequence 119 AA;
 Query Match 79.0%; Score 493; DB 2; Length 119;
 Best Local Similarity 81.5%; Pred. No. 1.5e-38;
 Matches 97; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
 QY 1 EVTLVESGGDFVKPGGSLKVCASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
 |||||
 Db 1 EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPKRLWVATISSGGYIYY 60
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMFYCTRVKLGTY--YFDSWGQGTTLTVSS 119
 |||||
 Db 61 PDSVKGRFTISRDNKNTLYLQMSLSRSDTAMYYCARRDYDLDFDSWGQGTTLTVSS 119
 RESULT 14
 ABP60555
 ID ABP60555 standard; protein; 134 AA.
 XX
 AC ABP60555;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Murine antibody 14F3 heavy chain variable region.
 XX
 KW Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;
 KW antiarthritic; antiinflammatory; cytostatic; antipsoriatic; antidiabetic;
 KW neuroprotective; gene therapy; rheumatoid arthritis; osteoporosis;
 KW bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis;

KW insuln-dependent diabetes; inflammatory bowel disease;
 KW multiple sclerosis; heavy chain variable region;
 KW complementary determining region; CDR.
 XX Mus musculus.
 XX
 FH Key Location/Qualifiers
 KW Region 31..35
 FT /label= CDR1
 FT Region 50..66
 FT /label= CDR2
 FT Region 99..110
 FT /label= CDR3
 XX
 PN WO200295012-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 03-MAY-2002; 2002WO-US014246.
 XX
 PR 18-MAY-2001; 2001US-0292031P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Sweet RW, Tornetta MA, Wattam TA;
 XX
 DR WPI; 2003-156758/15.
 DR N-PSDB; ABV99887.
 XX
 PT New monoclonal antibody having the characteristics of a monoclonal
 PT antibody 14F3, useful for treating or preventing osteopathic diseases,
 PT e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.
 PT psoriasis, or diabetes.
 XX
 PS Disclosure; Page 8; 51pp; English.
 XX
 CC The invention relates to a novel monoclonal antibody having the
 CC identifying characteristics of, or that is a monoclonal antibody 14F3. An
 CC antibody of the invention has osteopathic, antirheumatic, antiarthritic,
 CC antiinflammatory, cytostatic, antipsoriatic, antidiabetic, and
 CC neuroprotective activity. The polynucleotides encoding the antibodies of
 CC the invention may have a use in gene therapy. The antibodies and
 CC polypeptides are useful for treating or preventing osteopathic diseases,
 CC such as rheumatoid arthritis, osteoporosis, metastatic and primary bone
 CC cancer, wear debris induced osteolysis or osteoarthritis, and immune
 CC diseases such as psoriasis, insulin-dependent diabetes, inflammatory
 CC bowel disease or multiple sclerosis. The present sequence represents the
 CC heavy chain variable region of the murine monoclonal antibody 14F3 of the
 CC invention. The sequence contains three complementary determining regions
 CC (CDR's)
 XX
 SQ Sequence 134 AA;
 Query Match 78.0%; Score 487; DB 6; Length 134;
 Best Local Similarity 79.3%; Pred. No. 6.3e-38;
 Matches 96; Conservative 6; Mismatches 17; Indels 2; Gaps 1;
 QY 1 EVTLVESGGDFVKPGGSLKVCASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
 |||||
 Db 1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTY 60
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMFYCTRVKLGTY--YFDSWGQGTTLTVS 118
 |||||
 Db 61 PDSVKGRFTISRDNKNTLYLQMSLSRSDTAMYYCARLDGNYRWYFDWGTGTTTVTS 120
 QY 119 S 119
 Db 121 S 121
 RESULT 15
 AAB20442

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 9.03423 Seconds
(without alignments)
983.287 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EVTLVRSGGDFVKPGSLKV.....KLGTYVDFSWGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfileai.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	130	4	US-09-225-322B-18
2	624	100.0	130	4	US-09-764-304-18
3	614	98.4	130	4	US-09-225-322B-8
4	614	98.4	130	4	US-09-764-304-8
5	493	79.0	119	4	US-08-875-674A-1
6	486	77.9	247	5	PCT-US94-07659-2
7	480	76.9	119	4	US-08-875-674A-3
8	474	76.0	119	4	US-09-232-290-55
9	472	75.6	239	2	US-08-553-497A-18
10	469.5	75.2	135	3	US-08-579-378A-16
11	466.5	74.8	119	3	US-08-326-362-2
12	464	74.4	118	4	US-09-406-535-2
13	460.5	73.8	124	4	US-09-518-737-2
14	457.5	73.3	120	4	US-09-332-290-42
15	457.5	73.3	456	4	US-09-495-880A-11
16	457	73.2	217	5	PCT-US94-14106-59
17	453	72.6	119	4	US-09-648-067A-15
18	452	72.4	119	1	US-08-497-312-20
19	450.5	72.2	120	2	US-07-934-373C-4
20	450.5	72.2	120	3	US-08-437-642B-4
21	450.5	72.2	120	4	US-08-146-206C-4
22	450.5	72.2	120	4	US-09-705-686-4
23	450.5	72.2	120	4	US-09-705-392A-4
24	450.5	72.2	120	4	US-09-705-398-4
25	450	72.1	119	2	US-08-475-000-16
26	450	72.1	119	2	US-08-483-199-16
27	450	72.1	119	2	US-08-484-508-16

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Sequence 4, Appli
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Sequence 79, Appli
Sequence 75, Appli
Sequence 73, Appli
Sequence 6, Appli
Sequence 21, Appli
Sequence 21, Appli
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Sequence 3, Appli
Sequence 3, Appli
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Sequence 10, Appli
Sequence 84, Appli
Sequence 25, Appli
Sequence 6, Appli

ALIGNMENTS

```
RESULT 1
US-09-225-322B-18
; Sequence 18, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-18
Query Match      100.0%; Score 624; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 9.5e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
      |||
Db      11  EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQQTTLTVSS 119
      |||
Db      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQQTTLTVSS 129
      |||

RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
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; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-18
Query Match      100.0%; Score 624; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 9.5e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
      |||
Db      11  EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQQTTLTVSS 119
      |||
Db      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQQTTLTVSS 129
      |||

RESULT 3
US-09-225-322B-8
; Sequence 8, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8
Query Match      98.4%; Score 614; DB 4; Length 130;
Best Local Similarity 99.2%; Pred. No. 1.1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
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Db      11  EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAGISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQQTTLTVSS 119
      |||
Db      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQQTTLTVSS 129
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RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

Query Match          98.4%; Score 614; DB 4; Length 130;
Best Local Similarity 99.2%; Pred. No. 1.1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVTLVESGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLWVAYISSGSGTYY 60
Db 11 EVTLVESGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLWVAYISSGSGTYY 70

QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTTLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTTLTVSS 129

RESULT 5
US-08-875-674A-1
; Sequence 1, Application US/08875674A
; Patent No. 6572857
; GENERAL INFORMATION:
; APPLICANT: MONTERO CASIMIRO, J. B.
; APPLICANT: LOMBARDERO VALLADARES, J.
; APPLICANT: P REZ RODR GUEZ, R.
; APPLICANT: SIERRA BL ZQUEZ, P.
; APPLICANT: TORMO BRAVO, B. R.
; TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
; STREET: One Chase Road
; CITY: Scarsdale
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10583
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
; COMPUTER: Compatible PC IBM (80486, 8 M Ram).
```

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; OPERATING SYSTEM: Windows 95.
; SOFTWARE: Word Perfect 5.0 for Windows 95.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,674A
; FILING DATE: 17-July-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00004
; FILING DATE: 18-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: HENRY A. MARZULLO, JR.
; REGISTRATION NUMBER: 20,910
; REFERENCE/DOCKET NUMBER: P-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 723-4300
; TELEFAX: (914)-723-4301
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 Amino acid residues.
; TYPE: Amino acid.
; STRANDEDNESS: Unknown.
; TOPOLOGY: Unknown.
; MOLECULE TYPE: Protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: -N Terminal fragment.
; ORIGINAL SOURCE:
; ORGANISM: Mice Balb/C
; INDIVIDUAL ISOLATE: ior t1a
; TISSUE TYPE: Murine hibridoma
; IMMEDIATE SOURCE:
; CLONE: Sub-clone ior t1a
; FEATURE:
; IDENTIFICATION METHOD: Experimental.
; OTHER INFORMATION: Sequence corresponding to the variable region
; Patent No. 6572857
; OTHER INFORMATION: of the heavy chain of the monoclonal antibody recognizing hum
; OTHER INFORMATION: designated as sub-clone ior t1a.
US-08-875-674A-1

Query Match          79.0%; Score 493; DB 4; Length 119;
Best Local Similarity 81.5%; Pred. No. 1.1e-45;
Matches 97; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVTLVESGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLWVAYISSGSGTYY 60
Db 1 EVQLVESGGGLVPGGSLKLS CAASGFKFSRYAMSVWRQTPEKRLWVATISSGSGYIY 60

QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTTLTVSS 119
Db 61 PDSVKGRFTISRDNKNTLYLQWRSLSRSDTAMYYCARRDYDLDFDSWGQGTTLTVSS 119

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
```

ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 723-4300
TELEFAX: (914) 723-4301
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 Amino acid residues.
TYPE: Amino acid.
STRANDEDNESS: Unknown.
TOPOLOGY: Unknown.
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: -N Terminal fragment.
ORIGINAL SOURCE:
TISSUE TYPE: Animal cells.
CELL LINE: NSO " SP 2/0 " CHO
IMMEDIATE SOURCE:
CLONE: Sub-clone for t1A
FEATURE:
IDENTIFICATION METHOD: By similarity with known sequence.
OTHER INFORMATION: Sequence corresponding to the humanized
Patent No. 6572857
OTHER INFORMATION: variant of sub-clone for t1A recognizing human CD6, particularly
OTHER INFORMATION: to the variable region of its heavy chain.
US-08-875-674A-3

Query Match 77.9%; Score 486; DB 5; Length 247;
Best Local Similarity 79.0%; Pred No. 1.5e-44;
Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVCASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTY 60
DB 20 EVHVLVESGGGLVKPGGSLKSCAASGAFAPSSYDMSWVRQTPKRLDWVAYISSGGGTY 79
QY 61 SDSVKGRTTISRDNKNTLYLQMSLRSDSAMYFCTRVKLTGYFDSWGQTTLTVSS 119
DB 80 PDTVKGRTTISRDNKNTLYLQMSLRSDTAMVHCARGGVRGFDVWGAGTTVTVSS 138

RESULT 7
US-08-875-674A-3
Sequence 3, Application US/08875674A
Patent No. 6572857
GENERAL INFORMATION:
APPLICANT: MONTERO CASIMIRO, J. E.
APPLICANT: LOMBARDERO VALLADARES, J.
APPLICANT: P REZ RODR GUEZ, R.
APPLICANT: SIERRA BL ZQUEZ, P.
APPLICANT: TORMO BRAVO, B. R.
TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P. C.
STREET: One Chase Road
CITY: Scarsdale
STATE: New York
COUNTRY: U.S.A.
ZIP: 10583
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
COMPUTER: Compatible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM: Windows 95.
SOFTWARE: Word Perfect 5.0 for Windows 95.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,674A
FILING DATE: 17-July-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CU96/00004
FILING DATE: 18-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 723-4300
TELEFAX: (914) 723-4301
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 Amino acid residues.
TYPE: Amino acid.
STRANDEDNESS: Unknown.
TOPOLOGY: Unknown.
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: -N Terminal fragment.
ORIGINAL SOURCE:
TISSUE TYPE: Animal cells.
CELL LINE: NSO " SP 2/0 " CHO
IMMEDIATE SOURCE:
CLONE: Sub-clone for t1A
FEATURE:
IDENTIFICATION METHOD: By similarity with known sequence.
OTHER INFORMATION: Sequence corresponding to the humanized
Patent No. 6572857
OTHER INFORMATION: variant of sub-clone for t1A recognizing human CD6, particularly
OTHER INFORMATION: to the variable region of its heavy chain.
US-08-875-674A-3

Query Match 76.9%; Score 480; DB 4; Length 119;
Best Local Similarity 79.0%; Pred No. 2.8e-44;
Matches 94; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVCASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTY 60
DB 1 EVQLVESGGGLVKPGGSLKSCAASGAFKFSRYAMSWVRQAPGKRLWVATISSGGGTY 60
QY 61 SDSVKGRTTISRDNKNTLYLQMSLRSDSAMYFCTRVKLTGYFDSWGQTTLTVSS 119
DB 61 PDSVKGRTTISRDNKNTLYLQMSLRSDTAMVYCARRDYDLDFDSWGQTTLTVSS 119

RESULT 8
US-09-232-290-55
Sequence 55, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONEGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 55
LENGTH: 119
TYPE: PRI
ORGANISM: Murine
US-09-232-290-55

Query Match 76.0%; Score 474; DB 4; Length 119;
Best Local Similarity 77.3%; Pred No. 1.2e-43;
Matches 92; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGGSLKVCASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTY 60
DB 1 EVQLVESGGDLVKPGGSLKSCAASGFTFSRCAMSWVRQTPKRLWVAGISSGGGTY 60

QY 61 SDSVKGRTISRDNKNTLYLQMSLSRSDSAMVFCFTRVKLGTYYFDSWGQGTTLTVSS 119
Db 61 PDTVKGRTISRDNKNTLYLQMSLSRSDSAMVFCFTRVKLGTYYFDSWGQGTTLTVSS 119

RESULT 9
US-08-553-497A-18
; Sequence 18, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLERBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAM, JAUME
; APPLICANT: MITJANS, FRANCESSE
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-18

Query Match 75.6%; Score 472; DB 2; Length 239;
Best Local Similarity 77.3%; Pred. No. 4.8e-43;
Matches 92; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGAFAPSHYAMSVVROTPAKRLWEVAYISGGSGTTY 60
Db 1 EVKLQESGGDLVKPGGSLKLS CAASGFTFSSYGMVSVVROTDPKRLSVATISSGGAYIY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSLSRSDSAMVFCFTRVKLGTYYFDSWGQGTTLTVSS 119

Db 61 PSDVKGRFTISRDNKNTLYLQMSLSKSDTAMYYCARLETG DYALDYWGQGTTLTVSS 119

RESULT 10
US-08-579-378A-16
; Sequence 16, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-16

Query Match 75.2%; Score 469.5; DB 3; Length 135;
Best Local Similarity 79.8%; Pred. No. 4.4e-43;
Matches 95; Conservative 6; Mismatches 15; Indels 3; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGAFAPSHYAMSVVROTPAKRLWEVAYISGGSGTTY 60
Db 20 EVKLVESGGGLVKPGGSLKLA CAASGFTFSTYAMSVVROTPEKRLWEVASISGGS-TYY 78

QY 61 PSDVKGRFTISRDNKNTLYLQMSLSRSDSAMVFCFTRVKLGTYYFDSWGQGTTLTVSS 119
Db 79 PSDVKGRFTISRDNKNTLYLQMSLSRSDTAMYYCARDYDG--YFDYWGQGTTLTVSS 135

RESULT 11
US-08-326-362-2
; Sequence 2, Application US/08326362
; Patent No. 5730981
; GENERAL INFORMATION:

APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,362
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 08 795.3
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1276-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-326-362-2

Query Match 74.8%; Score 466.5; DB 1; Length 118;
Best Local Similarity 77.3%; Pred. No. 7.9e-43;
Matches 92; Conservative 7; Mismatches 19; Indels 1; Gaps 1;
Qy 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLWVAYISSGGSTYY 60
Db 1 QVQLQSGGGLVKPGGSLTSCAASRFTFTSYAMSWVRQTPAKRLWVAYISSGGASTYY 60
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRSEDSAMVCTRVKLGTYVDFDSWGQGTTLTVSS 119
Db 61 RDSVKGRTTISRDNKNTLYLQMSLSRSED TAMYCARQGVNFGIAY---WGQGTTLTVSS 118

RESULT 12
US-09-406-535-2
Sequence 2, Application US/09406535
Patent No. 6376653
GENERAL INFORMATION:
APPLICANT: Connie L. Erickson-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: James D. Winkler
TITLE OF INVENTION: Tie2 Antagonist Antibodies
FILE REFERENCE: P50844
CURRENT APPLICATION NUMBER: US/09/406,535
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 60/102,100
EARLIER FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2

LENGTH: 119
TYPE: PRT
ORGANISM: Mus musculus
US-09-406-535-2
Query Match 74.4%; Score 464; DB 3; Length 119;
Best Local Similarity 74.8%; Pred. No. 1.5e-42;
Matches 89; Conservative 8; Mismatches 22; Indels 0; Gaps 0;
Qy 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLWVAYISSGGSTYY 60
Db 1 EVQLVESGGGLVKPGGSLKLS CAASGFTFSDYGMHVRQAPEKGLWVAYINSGSSTYY 60
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRSEDSAMVCTRVKLGTYVDFDSWGQGTTLTVSS 119
Db 61 ADTVKGRFTISRDNKNTLYLQMTSLRSED TAIYICARGYGYPIFFDWGGTALT VSS 119
RESULT 13
US-09-518-737-2
Sequence 2, Application US/09518737
Patent No. 6709833
GENERAL INFORMATION:
APPLICANT: FUKUI, YASUHIISA
APPLICANT: NAGATA, SATOSHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
FILE REFERENCE: 1965/49618
CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 124
TYPE: PRT
ORGANISM: Mus musculus
US-09-518-737-2

Query Match 73.8%; Score 460.5; DB 4; Length 124;
Best Local Similarity 74.8%; Pred. No. 3.7e-42;
Matches 92; Conservative 7; Mismatches 17; Indels 7; Gaps 2;
Qy 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLWVAYISSGGSTYY 60
Db 1 EVQLVESGGDLVKPGGSLKLS CAASGFTFSSYGMWARQTPDKRLWVAYISSGGSTYY 60
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRSEDSAMVCTR---VKLGTYVDFDSWGQGTTLT 116
Db 61 PDSVKGRTTISRDNKNTLYLQMSLSRSED TAMYCARQGVNFGIAY---WGQGTTLTV 117
Qy 117 VSS 119
Db 118 VSA 120

RESULT 14
US-09-232-290-42
Sequence 42, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONEGGER, ANNE MARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
TITLE OF INVENTION: INCREASED SOLUBILITY
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230


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; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 120
; TYPE: PRN
; ORGANISM: Murine
US-09-232-290-42

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		Query Match	73.3%; Score 457.5; DB 4; Length 120;
		Best Local Similarity	75.8%; Pred. No. 7.5e-42;
		Matches 91; Conservative	8; Mismatches 20; Indels 1; Gaps 1;
Qy	1	EVTLVESGGDFVPGGSLKVCASAGGPAPHYAMSWRQTPTAKLEWVAISSGGSTYY	60
Dd	1	EVGLVESGGDLVKPGGSKLSCAASPFSFGSMWSVRQTPDKRELVATISNGGYTY	60
Qy	61	SDSVKGRTTISRDNKNTLYLOWRLSEDSAMYFCT-RVKLGITYYPDSVGCGTTLTVS	119
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Dd	61	PDSVKGRTTISRDNKNTLYLOWSLKSEDSAMYFCARRERYDENGFAFYQGTLTVSA	120
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RESULT 15

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US-09-495-880A-11
; Sequence 11, Application US/09495880A
; Patent No. 6667150
; GENERAL INFORMATION:
; APPLICANT: RUDERT, FRITZ
; APPLICANT: GE, LIMING
; APPLICANT: ILIAG, VIC
; TITLE OF INVENTION: NOVEL METHOD AND PHASE FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
; TITLE OF INVENTION: (POLY)PEPTIDE COMPLEX
; FILE REFERENCE: MORPHO/9
; CURRENT APPLICATION NUMBER: US/09/495,880A
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: PCT/EP98/04836
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: EP 97 11 3319.4
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-
; OTHER INFORMATION: HAG)-gene IIss encoded by phage vector flagla (circular)
US-09-495-880A-11

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	Best Local Similarity Matches	91;	Mismatches	8;	Conservative	20;	Gaps	1;
Qy		1	EVTLVESGGDFVKPGSLKVVSCAASGFAPSHYAMSWVRQTDPKRLEKWAVISSGSGTTY	60				
Dd		170	EVQLVESGGDLVFKPGSKLSCAAAGSFSSYGMSWVRQTDPDKRLEWATISNGGGSYYY	229				
Qy		61	SDSVGGRFTISRDNANKTLYLQMRSLSIEDSAAMYFCT-RVKLGITYYPDMSGQQTTLTIVSS	119				
Dd		230	PDSVKGRTISRDNANKTYLLQMSLKSDSAMIYCARRERYDENGFAYMGCGTTLTVSA	289				

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Job time : 10.0342 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 31.3976 Seconds
(without alignments)
1476.651 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EVTLVSGGDFVKPGSLKV.....KLGTYFDSWGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA:

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	624	100.0	130	14	US-10-265-713-18
3	624	100.0	130	14	US-10-166-626-18
4	614	98.4	130	9	US-09-764-304-8
5	614	98.4	130	14	US-10-265-713-8
6	614	98.4	130	14	US-10-166-626-8
7	487	78.0	134	16	US-10-477-377-3
8	486	77.9	140	13	US-10-006-773-4
9	481	77.1	121	15	US-10-276-939-3
10	477	76.4	232	18	US-10-511-794-17
11	477	76.4	241	18	US-10-511-794-16
					Sequence 18, Appl
					Sequence 18, Appl
					Sequence 8, Appl
					Sequence 8, Appl
					Sequence 3, Appl
					Sequence 3, Appl
					Sequence 17, Appl
					Sequence 16, Appl

85 453 72.6 119 15 US-10-608-626-6 Sequence 6, Appli
86 453 72.6 119 15 US-10-600-152-15 Sequence 15, Appli
87 453 72.6 119 15 US-10-619-754-6 Sequence 6, Appli
88 453 72.6 119 16 US-10-719-310-6 Sequence 6, Appli
89 453 72.6 119 17 US-10-861-049-42 Sequence 42, Appli
90 453 72.6 120 17 US-10-938-353-104 Sequence 104, App
91 453 72.6 121 15 US-10-447-331-4 Sequence 4, Appli
92 453 72.6 269 13 US-10-027-770-2 Sequence 60, Appli
93 452 72.4 119 14 US-10-281-479A-60 Sequence 60, Appli
94 452 72.4 119 14 US-10-275-180A-60 Sequence 60, Appli
95 452 72.4 119 14 US-10-286-132A-60 Sequence 60, Appli
96 452 72.4 269 13 US-10-027-770-5 Sequence 5, Appli
97 452 72.4 451 16 US-10-679-620-78 Sequence 78, Appli
98 452 72.4 512 16 US-10-679-620-70 Sequence 70, Appli
99 452 72.4 517 16 US-10-679-620-68 Sequence 68, Appli
100 452 72.4 519 16 US-10-679-620-66 Sequence 66, Appli

ALIGNMENTS

RESULT 1

US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-18
Query Match 100.0%; Score 624; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.8e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGSLKSCAAGFAPSHYAMSWVRQTPAKRLEWYAYISGGSGGY 60
Db 11 EVTLVESGGDFVKPGSLKSCAAGFAPSHYAMSWVRQTPAKRLEWYAYISGGSGGY 70
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 119
Db 71 SDSVKGRTTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 129

RESULT 2

US-10-265-713-18
; Sequence 18, Application US/10265713
; Patent No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; EARLIER APPLICATION NUMBER: US/09/225,322B
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
US-10-166-626-18
; Sequence 18, Application US/10166626
; Patent No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; EARLIER APPLICATION NUMBER: US/09/225,322B
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19


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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-8

Query Match
Best Local Similarity 98.4%; Score 614; DB 14; Length 130;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
Db 11 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAGISSGGSGTY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFDSWGQGTTLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFDSWGQGTTLTVSS 129

RESULT 7
US-10-477-377-3
; Sequence 3, Application US/10477377
; Publication No. US20040213788A1
; GENERAL INFORMATION:
; APPLICANT: Sweet, Raymond
; APPLICANT: Tornetta, Mark
; APPLICANT: Wattam, Trevor
; TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
; FILE REFERENCE: GP50050
; CURRENT APPLICATION NUMBER: US/10/477,377
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US02/14246
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/292,031
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-477-377-3

Query Match
Best Local Similarity 78.0%; Score 487; DB 16; Length 134;
Matches 96; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
Db 1 EVQLVESGDDLVPKPGSLKLS CAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
Db 61 PDSVKGRFTISRDNKNTLYLQMRSLKSEDTAMYYCARLDGYNRYRWYFDVWVGTTTVTS 120
QY 119 $ 119
Db 121 $ 121

RESULT 8
US-10-006-773-4
; Sequence 4, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
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; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-4

Query Match
Best Local Similarity 77.9%; Score 486; DB 13; Length 140;
Matches 94; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
Db 20 EVVVESGGDFVKPGGSLKLS CAAGFTFSRYAMSWVRQTPKRLWVATISSGGSHY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR--VKLGTYYFDSWGQGTTLTVS 118
Db 80 PDSVKGRFTISRDNKNTLYLQMRSLRSEDTAIYYCARPGYDRGAWFFDVWVGTTTVTS 139
QY 119 $ 119
Db 140 $ 140

RESULT 9
US-10-276-939-3
; Sequence 3, Application US/10276939
; Publication No. US20030215450A1
; GENERAL INFORMATION:
; APPLICANT: BLAKE, SIMON M.
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TAYLOR, ALEXANDER H.
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
; FILE REFERENCE: GP50024
; CURRENT APPLICATION NUMBER: US/10/276,939
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/US01/16865
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,628
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Murine
US-10-276-939-3

Query Match
Best Local Similarity 77.1%; Score 481; DB 15; Length 121;
Matches 95; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
Db 1 EVQLVESGDDLVPKPGGSLKLS CAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
Db 61 PDSVKGRFTISRDNKNTLYLQMRSLKSEDTAMYYCARLDGYNRYRWYFDVWVGTTTVTS 120
QY 119 $ 119
Db 121 $ 121

RESULT 10
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US-10-511-794-17
; Sequence 17, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN (CEA)
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511,794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: diabody
US-10-511-794-17

Query Match          76.4%; Score 477; DB 18; Length 232;
Best Local Similarity 79.2%; Pred. No. 2.3e-36;
Matches 95; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVTLVSGGDFVKPGGSLKVSACGAFASHYAMSWVROTPAKRLEWVAIISGGSTYY 60
   |||||
Db 1 EVKLVSAGDLVXPGGSLKVSACGAFASHYAMSWVROTPEKRLEWVAIISDGI-AYY 59
   |||||

QY 61 SDSVKGRTISRDNARNTLYLQMSLRSEDSAMYFCTRV-KLGTYYFDSWGQGTTLTVSS 119
   :|||
Db 60 ADSVKGRTISRDNARNTLYLQMSLRSEDSAMYCARVYVYSSYFDYWGQGTTLTVSS 119

RESULT 11
US-10-511-794-16
; Sequence 16, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN (CEA)
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511,794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv
US-10-511-794-16

Query Match          76.4%; Score 477; DB 18; Length 241;
Best Local Similarity 79.2%; Pred. No. 2.4e-36;
Matches 95; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVTLVSGGDFVKPGGSLKVSACGAFASHYAMSWVROTPAKRLEWVAIISGGSTYY 60
   |||||
Db 1 EVKLVSAGDLVXPGGSLKVSACGAFASHYAMSWVROTPEKRLEWVAIISDGI-AYY 59
   |||||

QY 61 SDSVKGRTISRDNARNTLYLQMSLRSEDSAMYFCTRV-KLGTYYFDSWGQGTTLTVSS 119
   :|||
Db 60 ADSVKGRTISRDNARNTLYLQMSLRSEDSAMYCARVYVYSSYFDYWGQGTTLTVSS 119
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RESULT 12
US-10-511-794-21
; Sequence 21, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN (CEA)
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511,794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: diabody MS
US-10-511-794-21

Query Match          76.4%; Score 477; DB 18; Length 255;
Best Local Similarity 79.2%; Pred. No. 2.5e-36;
Matches 95; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVTLVSGGDFVKPGGSLKVSACGAFASHYAMSWVROTPAKRLEWVAIISGGSTYY 60
   |||||
Db 1 EVKLVSAGDLVXPGGSLKVSACGAFASHYAMSWVROTPEKRLEWVAIISDGI-AYY 59
   |||||

QY 61 SDSVKGRTISRDNARNTLYLQMSLRSEDSAMYFCTRV-KLGTYYFDSWGQGTTLTVSS 119
   :|||
Db 60 ADSVKGRTISRDNARNTLYLQMSLRSEDSAMYCARVYVYSSYFDYWGQGTTLTVSS 119

RESULT 13
US-10-281-479A-61
; Sequence 61, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: artificial sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthetic
US-10-281-479A-61

Query Match 76.1%; Score 475; DB 14; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.7e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFVKPGGSLKVCASGPAFASHVAMSWVRQTPAKRLEWVAYISSGGSGTY 60
Db 1 EYMLVESGGGLVKPGGSLKVCASGFTFSSVYMSWVRQTPKRLWVATISSGGSYTY 60

QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYVFDWSGQGTTLTVSS 119
Db 61 PDSVKGRTISRDNKNTLYLQMSLRSEDTAMYICARRGDSMITTDYWGQGTTLTVSS 119

RESULT 14
US-10-275-180A-61
; Sequence 61, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U5
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e = Synthetic Construct
US-10-275-180A-61

Query Match 76.1%; Score 475; DB 14; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.7e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFVKPGGSLKVCASGPAFASHVAMSWVRQTPAKRLEWVAYISSGGSGTY 60
Db 1 EYMLVESGGGLVKPGGSLKVCASGFTFSSVYMSWVRQTPKRLWVATISSGGSYTY 60

QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYVFDWSGQGTTLTVSS 119
Db 61 PDSVKGRTISRDNKNTLYLQMSLRSEDTAMYICARRGDSMITTDYWGQGTTLTVSS 119

RESULT 15
US-10-286-132A-61
; Sequence 61, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthetic Construct
US-10-286-132A-61

Query Match 76.1%; Score 475; DB 14; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.7e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFVKPGGSLKVCASGPAFASHVAMSWVRQTPAKRLEWVAYISSGGSGTY 60
Db 1 EYMLVESGGGLVKPGGSLKVCASGFTFSSVYMSWVRQTPKRLWVATISSGGSYTY 60

QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYVFDWSGQGTTLTVSS 119
Db 61 PDSVKGRTISRDNKNTLYLQMSLRSEDTAMYICARRGDSMITTDYWGQGTTLTVSS 119

Search completed: August 1, 2005, 09:28:03
Job time : 32.3976 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.73864 Seconds
(without alignments)
1699.125 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EVTLVSGGDFVXPGSLKV.....KLGTYYFDSWGQTTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	479	76.8	119	2 B34353	anti-peptide Fab'
2	471	75.5	120	2 S55336	Ig heavy chain V r
3	470.5	75.4	121	2 I27887	Ig heavy chain V r
4	469	75.2	120	2 S55337	Ig heavy chain V r
5	469	75.2	122	2 E27888	Ig heavy chain V r
6	467	74.8	111	2 PH1007	Ig heavy chain V r
7	466.5	74.8	119	2 F27888	Ig heavy chain V r
8	464	74.4	138	2 S09258	Ig heavy chain V r
9	463	74.2	120	2 S55339	Ig heavy chain V r
10	462.5	74.1	118	2 PH0097	Ig heavy chain V r
11	462	74.0	118	2 S20641	Ig heavy chain V r
12	461	73.9	117	2 PL0249	Ig heavy chain V r
13	460	73.7	120	2 S55338	Ig heavy chain V r
14	457.5	73.3	254	2 B31790	Ig heavy chain V r
15	456.5	73.2	118	2 PH0096	Ig heavy chain V r
16	456	73.1	119	2 S31107	Ig heavy chain V r
17	456	73.1	124	2 C27888	Ig heavy chain - h
18	456	73.1	138	2 S31666	Ig heavy chain V r
19	455.5	73.0	112	2 S26327	Ig heavy chain V r
20	454	72.8	117	2 PL0252	Ig heavy chain V r
21	452.5	72.5	121	2 A27888	Ig heavy chain V r
22	452.5	72.5	121	2 S55340	Ig heavy chain V r
23	451.5	72.4	121	2 D27888	Ig heavy chain V r
24	451.5	72.4	121	2 B27888	Ig heavy chain V r
25	450.5	72.2	119	2 D27889	Ig heavy chain V r
26	449.5	72.0	113	2 S26468	Ig heavy chain V r
27	449.5	72.0	121	2 H27887	Ig heavy chain V r
28	448.5	71.9	139	2 S38808	Ig heavy chain - m
29	447.5	71.7	548	2 S38864	Ig epsilon chain

30	447	71.6	152	2 B26471	Ig heavy chain pre
31	446.5	71.6	128	2 S26790	Ig heavy chain V r
32	444.5	71.2	119	2 B27889	Ig heavy chain V r
33	443.5	71.1	121	2 H27888	Ig heavy chain V r
34	443	71.0	119	2 PH0098	Ig heavy chain V r
35	442	70.8	124	2 I27888	Ig heavy chain V r
36	441.5	70.8	108	2 PH1010	Ig heavy chain (su
37	441.5	70.8	118	2 S31105	Ig heavy chain V r
38	441	70.7	119	2 D36005	Ig heavy chain V r
39	440	70.5	125	2 S30531	Ig heavy chain V r
40	439.5	70.4	120	2 S12953	Ig heavy chain V r
41	439.5	70.4	123	2 S63597	Ig heavy chain, v
42	439	70.4	119	2 S31108	Ig heavy chain - h
43	438.5	70.3	123	2 G27888	Ig heavy chain V r
44	438	70.2	140	2 S31686	Ig heavy chain V r
45	437.5	70.1	140	2 S70442	Ig heavy chain pre
46	437	70.0	160	2 S05271	Ig heavy chain pre
47	436.5	70.0	119	2 PH1531	Ig H chain V regio
48	436.5	70.0	122	2 PH1537	Ig H chain V regio
49	435	69.7	123	2 S31114	Ig heavy chain - h
50	434	69.6	123	2 S26794	Ig heavy chain V r
51	434	69.6	213	2 S68213	Ig heavy chain (Ma
52	432.5	69.3	106	2 PH1008	Ig heavy chain V r
53	432.5	69.3	108	2 PL0248	Ig heavy chain V r
54	432.5	69.3	114	2 S31120	Ig heavy chain - h
55	432.5	69.3	120	2 S44111	Ig heavy chain V-D
56	432.5	69.3	124	2 S20782	Ig heavy chain V r
57	431.5	69.2	111	2 PL0199	anti-DNA autoantib
58	431.5	69.2	128	2 S26786	Ig heavy chain V r
59	431.5	69.2	137	2 S78054	Ig heavy chain pre
60	431	69.1	117	1 HVMS34	Ig heavy chain pre
61	430	68.9	119	2 A43413	Ig heavy chain V r
62	429.5	68.8	112	2 A27889	Ig heavy chain V r
63	429.5	68.8	128	2 PH0095	Ig kappa chain V r
64	429.5	68.8	147	2 I37780	Ig variable region
65	429	68.8	119	2 C36005	Ig heavy chain V r
66	429	68.8	135	2 S31598	Ig heavy chain V r
67	429	68.8	139	2 I37781	Ig variable region
68	429	68.8	140	2 S31588	Ig heavy chain V r
69	428.5	68.7	120	2 S48798	Ig heavy chain V r
70	428.5	68.7	120	2 E49590	Ig heavy chain V r
71	428.5	68.7	139	2 S31674	Ig heavy chain V r
72	427.5	68.5	141	2 S31669	Ig heavy chain V r
73	427	68.4	119	2 F36005	Ig heavy chain V r
74	427	68.4	143	2 S23624	Ig heavy chain V r
75	425.5	68.2	128	2 PH0094	Ig heavy chain V r
76	425.5	68.2	135	2 I37778	Ig variable region
77	425	68.1	108	2 PH1006	Ig heavy chain V r
78	425	68.1	142	2 C34903	Ig heavy chain pre
79	424.5	68.0	136	2 S31587	Ig heavy chain V r
80	424	67.9	124	2 S20784	Ig heavy chain V r
81	424	67.9	127	2 S38489	Ig heavy chain - h
82	423.5	67.9	120	2 PH1534	Ig H chain V regio
83	423.5	67.9	122	2 E36005	Ig heavy chain V r
84	423.5	67.9	136	1 GLMS21	Ig heavy chain pre
85	423	67.8	121	2 G34871	Ig heavy chain V r
86	422.5	67.7	122	2 S20772	Ig heavy chain V r
87	422	67.6	123	2 S38493	Ig heavy chain - h
88	422	67.6	134	2 S31699	Ig heavy chain V r
89	421.5	67.5	122	2 PC2398	anti-tetanus toxin
90	421	67.5	121	2 G36005	Ig heavy chain V r
91	421	67.5	132	2 S31603	Ig heavy chain V r
92	420.5	67.4	119	2 PH1533	Ig H chain V regio
93	420	67.3	134	2 S31679	Ig heavy chain V r
94	419	67.1	111	2 S40090	Ig heavy chain - m
95	419	67.1	117	2 S78486	Ig heavy chain V r
96	419	67.1	121	2 I55673	Ig heavy chain - h
97	419	67.1	121	2 S19666	Ig heavy chain V r
98	418.5	67.1	110	2 PH1652	Ig heavy chain V r
99	418.5	67.1	114	2 PH1009	Ig heavy chain V r
100	417.5	66.9	128	2 S48797	Ig heavy chain V r

ALIGNMENTS

```

RESULT 1
B34353
anti-peptide Fab' B3I12 heavy chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 23-Jul-1999
C;Accession: B34353
R;Stura, E.A.; Scanfield, R.L.; Fieser, T.M.; Balderas, R.S.; Smith, L.R.; Lerner, R.A.; J. Biol. Chem. 264, 15721-15725, 1989
A;Title: Preliminary crystallographic data and primary sequence for anti-peptide Fab' B3I12
A;Reference number: A34353; MUID:89359424; PMID:2504725
A;Accession: B34353
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <STU>
A;Cross-references: GB:M29252; NID:g195657; PIDN:AAA38388.1; PID:g195658
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      76.8%; Score 479; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.3e-37;
Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSVWRQTPAKRLWAVYISSGGSGTTY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 EQVLVESGGDLVKGPSLKLSCAASGTFTRCAMSVWRQTPEAKRLWAVAGISSGSYTFF 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNAXNTLYQLMSLRSEDSAMYFCFRVKLGTYTYPFDSWGQGTTLTSS 119
   .||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 PDTVKGRFTISRDNARNTLSLQMSLRSEDTAIYCTRYSSDPFYFDYWGQGTTLTSS 119
   .||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
S55536
Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55536
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A. J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin-
       ations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55536
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match      75.5%; Score 471; DB 2; Length 120;
Best Local Similarity 78.3%; Pred. No. 7.1e-37;
Matches 94; Conservative 5; Mismatches 19; Indels 2; Gaps 1;

QY 2 VTLLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSVWRQTPAKRLWAVYISSGGSGTYYS 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 VLQLESGGGLVKPGGSLKLS CAASGTFTRCYAMSVWRQTPEKRLWAVATISSGSYTYP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 62 DSVKGRFTISRDNAXNTLYQLMSLRSEDSAMYFCFTRV--KLGTYYFDSWGQGTTLTVSS 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 DSVKGRFTISRDNAXNTLYQLMSLRSEDTAMYYCARLYVDYDYPVMYWGQGTTLTVSS 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
I27887
Ig heavy chain V region (H37-45) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: I27887

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R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a de
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: I27887
A;Molecule type: DNA
A;Residues: 1-121 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 470.5; DB 2; Length 121;
Best Local Similarity 76.9%; Pred. No. 8e-37;
Matches 93; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

Qy 1 EVTLVESGGDFVKPGGSLKVCSCAASGFAFSSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
Db 1 EVMLVESGGGLVKPGGSLKLSCAASGFTFSYAMSWVRQTPKRLEWVATISSGGSTY 60
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYCFTR---VKLGTYFFDSWGQGTTLTV 117
Db 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDTAMYCYCARBEGLRLEDYANDYWGQGTSTV 120
Qy 118 S 118
Db 121 S 121

RESULT 4
S55537
Ig heavy chain V region pe21 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55537
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55537
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82590; NID:9854306; PIDN:CAAS7926.1; PID:9854307
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 469; DB 2; Length 120;
Best Local Similarity 78.3%; Pred. No. 1.1e-36;
Matches 94; Conservative 5; Mismatches 19; Indels 2; Gaps 1;

Qy 2 VTLVESGGDFVKPGGSLKVCSCAASGFAFSSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 61
Db 1 VQLQESGGGLVKPGGSLKLSCAASRFTFSYAMSWVRQTPKRLEWVATISSGGSTY 60
Qy 62 DSVKGRFTISRDNKNTLYLQMSLRSEDSAMYCFTRV---KLGTYFFDSWGQGTTLTVSS 119
Db 61 DSVKGRFTISRDNKNTLYLQMSLRSEDTAMYCYCTRLYYDYPVMDYWGQGTTLTVSS 120

RESULT 5
E27888
Ig heavy chain V region (H35-C6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: E27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a de

A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: E27888

A;Molecule type: DNA

A;Residues: 1-122 <CAT>

A;Experimental source: strain Balb/c

A;Note: this sequence was determined from the germline gene

C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus H

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 469; DB 2; Length 122;
Best Local Similarity 75.4%; Pred. No. 1.1e-36;
Matches 92; Conservative 8; Mismatches 18; Indels 4; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 1 DVKLVESGGGLVKPGGSLKLS CAASGFTFSYTMVSRQTPKRLWVAIISGGSYTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTR----VKLGYTFYFDSWGQGTTLT 116

Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRQGEYRYYDDYAMDYWGQGTSTV 120

QY 117 VS 118

Db 121 VS 122

RESULT 6

PH1007

IG heavy chain V region (clone 163-cl) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1007

R;Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1007

A;Molecule type: mRNA

A;Residues: 1-111 <TL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 467; DB 2; Length 111;
Best Local Similarity 82.0%; Pred. No. 1.5e-36;
Matches 91; Conservative 3; Mismatches 15; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 1 EVKLVESGGGLVKPGGSLKLS CAASGFTFSYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTRVLG--TYFDSW 109

Db 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDTAMTYCASHYVGRTYTFDYW 111

RESULT 7

F27888

IG heavy chain V region (H158-89H4) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C;Accession: F27888

R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A;Title: Structural and functional implications of a restricted antibody response to a c

A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: F27888

A;Molecule type: DNA

A;Residues: 1-119 <CAT>

A;Experimental source: strain Balb/c

A;Note: this sequence was determined from the germline gene

C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus he

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 466.5; DB 2; Length 119;
Best Local Similarity 76.9%; Pred. No. 1.8e-36;
Matches 93; Conservative 8; Mismatches 15; Indels 5; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 1 DVKLVESGGGLVKPGGSLKLS CAASGFTFSYTMVSRQTPKRLWVAIISGGSYTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTRVLKGY--PDSWGQGTTLTV 117

Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMTYCPRG--TYDYAMDYWGQGTSTV 118

QY 118 S 118

Db 119 S 119

RESULT 8

S09258

IG heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRX1

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:G53207; PIDN:CAA36012.1; PID:G297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 464; DB 2; Length 138;
Best Local Similarity 75.6%; Pred. No. 3.7e-36;
Matches 90; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 20 EVILVESGGGLVKPGGSLKLS CAASGFTFSYTMVSRQTPKRLWVAIISGGGNTYY 79

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTRVLKGYTFPDSWGQGTTLTVSS 119

Db 80 PDSVKGRFTISRDNKNTLYLQMSLSRSDTALYCARYRYEAFASWGQGTTLTVSA 138

RESULT 9

S55539

IG heavy chain V region pc24 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C;Accession: S55539

R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

utations in the variable region genes.

A;Reference number: S55528; MUID:95239763; PMID:7536850

A;Accession: S55539

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <BOE>

A;Cross-references: EMBL:X82593; NID:G854312; PIDN:CAA57929.1; PID:G854313

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 463; DB 2; Length 120;
Best Local Similarity 76.7%; Pred. No. 3.9e-36;
Matches 92; Conservative 6; Mismatches 20; Indels 2; Gaps 1;

QY 2 VTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTYYS 61
DB 1 VQLQSSGGGLVKPGGSLKLS CAASGFTFSYAMSWVRQTPKRLWVATISSGGGTYYP 60
QY 62 DSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRV--KLGTYYFDSWGQTTTLTVSS 119
DB 61 DSVKGRFTISRDNKNTLYLQMSRLSRSDTAMYYCRLYYDYDPYMDYWGQTTTLTVSS 120

RESULT 10

PH0097
Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C:Accession: PH0097
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koher, H.P.; Quesniaux, V.F.J.; V
Mol. Immunol. 27, 1029-1038, 1990
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A:Reference number: PH0087; MUID:91042849; PMID:2122240
A:Accession: PH0097
A:Molecule type: mRNA
A:Residues: 1-118 <SCH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:50-66/Region: complementarity-determining 2
F:99-105/Region: complementarity-determining 3

Query Match 74.1%; Score 462.5; DB 2; Length 118;
Best Local Similarity 79.0%; Pred. No. 4.3e-36;
Matches 94; Conservative 4; Mismatches 18; Indels 3; Gaps 1;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTYYY 60
DB 1 DVKLVESGGGLVKPGGSLKLS CAASGFTFSYIMSWVRQTPKRLWVATISSGGGTYYY 60
QY 61 DSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRVKGTYTFDSWGQTTTLTVSS 119
DB 61 DSVKGRFTISRDNKNTLYLQMSRLSRSDTAMYYST---ASGDSFDYWGQTTTLTVSS 116

RESULT 11

S20641
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20641
R:Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A:Reference number: S20639
A:Accession: S20641
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <LOS>
A:Cross-references: EMBL:X65003; NID:G52602; PIDN:CAA46136.1; PID:G52603
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 462; DB 2; Length 118;
Best Local Similarity 75.4%; Pred. No. 4.8e-36;
Matches 89; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTYYY 60
DB 1 EVKLVESGGGLVKPGGSLKLS CAASGFTFSYIMFWVRQTPAKRLEWVATISSGGGTYYY 60
QY 61 DSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRVKGTYTFDSWGQTTTLTVS 118
DB 61 PDSVKGRFTISRDNVNMNITLYLQMSRLSRSDTAMYYCARRAYSNVALDFWGQGTSTVTS 118

RESULT 12

PL0249
Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0249
R:Shiomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0249
A:Molecule type: mRNA
A:Residues: 1-117 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-108/Region: complementarity-determining 3
F:109-117/Region: framework 4

Query Match 73.9%; Score 461; DB 2; Length 117;
Best Local Similarity 75.2%; Pred. No. 5.9e-36;
Matches 88; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTYYY 60
DB 1 EVKLVESGGGLVKPGGSLKLS CAASGFTFSYIMSWVRQTPAKRLEWVATISSGGGTYYY 60
QY 61 DSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRVKGTYTFDSWGQTTTLTV 117
DB 61 PDSVKGRFTISRDNARNTLYLQMSRLSRSDTAMYYCARRDYSHWFFDVWGAGTTTV 117

RESULT 13

S55538
Ig heavy chain V region pe22 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55538
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55538
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <BOE>
A:Cross-references: EMBL:X82591; NID:G854308; PIDN:CAA57927.1; PID:G854309
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 460; DB 2; Length 120;
Best Local Similarity 75.8%; Pred. No. 7.5e-36;
Matches 91; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

QY 2 VTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLEWVAYISSGGGTYYS 61
DB 1 VKLQSSGGGLVKPGGSLKLS CAASGFTFSYAMSWVRQTPKRLWVATISSGGGTYYP 60

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 30.8793 Seconds
(without alignments)
1973.408 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EYTLVSGGDFVKPGSLKV.....KLGTYFYDSMGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	75.2	255	2	Q6KB05 mus musculus
2	468.5	75.1	487	2	Q99KA4 mus musculus
3	463	74.2	119	2	Q920E7 mus musculus
4	455	72.9	486	2	Q91207 mus musculus
5	450	72.1	479	2	Q91WP5 mus musculus
6	439.5	70.4	473	2	Q91205 mus musculus
7	431.5	69.2	606	2	Q6GMY2 mus musculus
8	431	69.1	117	1	Q9UL71 mus musculus
9	430	68.9	121	2	Q9UL71 mus musculus
10	429	68.8	480	2	Q91XEL mus musculus
11	426	68.3	136	2	Q65ZL8 mus musculus
12	426	68.3	478	2	Q6PI81 mus musculus
13	425	68.1	464	2	Q6MZU6 mus musculus
14	424	67.9	485	2	Q6PDB8 mus musculus
15	423.5	67.9	136	1	HV16_MOUSE
16	419.5	67.2	465	2	HV16_MOUSE
17	417	66.8	117	1	HV54_MOUSE
18	417	66.8	470	2	Q6PUA4 mus musculus
19	414.5	66.4	97	1	HV56_MOUSE
20	414.5	66.4	118	2	Q9UL91 mus musculus
21	413	66.2	248	2	Q65Q07 mus musculus
22	413	66.2	493	2	Q6GMX2 mus musculus
23	412.5	66.1	613	2	Q8WUK1 mus musculus
24	410	65.7	113	2	Q9UL90 mus musculus
25	410	65.7	597	2	Q96BB9 mus musculus
26	407.5	65.3	118	2	Q9UL72 mus musculus
27	407.5	65.3	494	2	Q96K68 mus musculus
28	407	65.2	198	1	HV57_MOUSE
29	406	65.1	117	1	HV58_MOUSE
30	406	65.1	240	2	Q65ZC9 mus musculus
31	405	64.9	116	2	Q9UL93 mus musculus

32	404.5	64.8	473	2	Q6MZV7	Q6mzv7 homo sapien
33	403.5	64.7	475	2	Q6MZQ6	Q6mzq6 homo sapien
34	401.5	64.3	122	1	HV3Q_HUMAN	P01768 homo sapien
35	400.5	64.2	573	2	Q8WU38	Q8w38 homo sapien
36	399.5	64.0	471	2	Q66K04	Q66k04 mus musculus
37	398	63.8	499	2	Q8NSK4	Q8nsk4 homo sapien
38	397.5	63.7	112	2	Q9HCC1	Q9hcc1 homo sapien
39	396	63.5	472	2	Q6N089	Q6n089 homo sapien
40	395.5	63.4	147	2	Q9Y509	Q9y509 homo sapien
41	393.5	63.1	122	2	Q9UL84	Q9ul84 homo sapien
42	391.5	62.7	119	1	HV38_MOUSE	P01808 mus musculus
43	391.5	62.7	479	2	Q6MZV6	Q6mzv6 homo sapien
44	391	62.7	121	1	HV3J_HUMAN	P01771 homo sapien
45	390.5	62.6	475	2	Q6GMW7	Q6gmw7 homo sapien
46	390	62.5	117	1	HV59_MOUSE	P18530 mus musculus
47	390	62.5	493	2	Q8NCL6	Q8nc16 homo sapien
48	389.5	62.4	484	2	Q8VEA0	Q8vea0 mus musculus
49	389	62.3	487	2	Q80Z17	Q80z17 mus musculus
50	387.5	62.1	122	1	HV3A_HUMAN	P01762 homo sapien
51	387.5	62.1	487	2	Q6ZVX0	Q6zvxo homo sapien
52	385	61.7	117	1	HV02_CANFA	P01785 canis fam1
53	385	61.7	117	1	HV3C_HUMAN	P01764 homo sapien
54	383.5	61.5	116	1	HV3T_HUMAN	P01781 homo sapien
55	383	61.4	119	1	HV3I_HUMAN	P01770 homo sapien
56	383	61.4	480	2	Q6N094	Q6n094 homo sapien
57	382	61.2	115	1	HV3D_HUMAN	P01765 homo sapien
58	382	61.2	118	1	HV39_MOUSE	P01809 mus musculus
59	381	61.1	466	2	Q6IN78	Q6in78 homo sapien
60	380.5	61.0	126	1	HV3K_HUMAN	P01772 homo sapien
61	380	60.9	117	1	HV53_MOUSE	P18534 mus musculus
62	378.5	60.7	114	1	HV3B_HUMAN	P01763 homo sapien
63	378.5	60.7	544	2	Q6PJ95	Q6pj95 homo sapien
64	377.5	60.5	483	2	Q6MZX9	Q6mzx9 homo sapien
65	376.5	60.3	122	1	HV20_MOUSE	P01789 mus musculus
66	375	60.1	115	1	HV3F_HUMAN	P01767 homo sapien
67	374.5	60.0	114	1	HV01_CANFA	P01784 canis fam1
68	371.5	59.5	122	1	HV3H_HUMAN	P01769 homo sapien
69	370.5	59.4	111	1	HV35_MOUSE	P01804 mus musculus
70	370.5	59.4	494	2	Q6ZM64	Q6zm64 homo sapien
71	370	59.3	119	1	HV3L_HUMAN	P01773 homo sapien
72	370	59.3	120	1	HV3E_HUMAN	P01766 homo sapien
73	367.5	58.9	122	1	HV21_MOUSE	P01790 mus musculus
74	367	58.8	123	1	HV18_MOUSE	P01787 mus musculus
75	366.5	58.7	116	1	HV05_CARAU	P19181 carassius a
76	366.5	58.7	120	1	HV3U_HUMAN	P01782 homo sapien
77	366.5	58.7	298	2	Q9QYF0	Q9qyf0 synthetic c
78	366	58.7	466	2	Q6N096	Q6n096 homo sapien
79	365	58.5	123	1	HV19_MOUSE	P01788 mus musculus
80	364.5	58.4	119	1	HV37_MOUSE	P01807 mus musculus
81	364	58.3	123	1	HV23_MOUSE	P01792 mus musculus
82	363	58.2	117	1	HV41_MOUSE	P01811 mus musculus
83	363	58.2	144	1	HV26_MOUSE	P01795 mus musculus
84	362.5	58.1	614	2	Q6DDQ7	Q6ddq7 xenopus lae
85	362	58.0	464	2	Q6PIP8	Q6pip8 mus musculus
86	361.5	57.9	473	2	Q6P055	Q6p055 homo sapien
87	361	57.9	123	1	HV24_MOUSE	P01793 mus musculus
88	360	57.7	123	1	HV25_MOUSE	P01794 mus musculus
89	359	57.5	95	2	Q9UL56	Q9ulb6 homo sapien
90	359	57.5	123	1	HV22_MOUSE	P01791 mus musculus
91	358.5	57.5	119	1	HV3N_HUMAN	P01775 homo sapien
92	358	57.4	115	1	HV32_MOUSE	P01801 mus musculus
93	358	57.4	519	2	HV30_MOUSE	Q6n092 homo sapien
94	357.5	57.3	119	1	HV3M_HUMAN	P01774 homo sapien
95	357	57.2	131	2	Q9UL38	Q9ul88 homo sapien
96	357	57.2	470	2	Q725W1	Q725w1 homo sapien
97	355	56.9	458	2	Q65ZQ1	Q65zq1 homo sapien
98	355	56.9	593	2	Q6INM5	Q6inm5 xenopus lae
99	354.5	56.8	119	1	HV40_MOUSE	P01810 mus musculus
100	353	56.6	117	1	HV42_MOUSE	P01812 mus musculus

ALIGNMENTS

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RESULT 1
Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE SCFV B8E5 protein (Fragment).
GN Name=SCFV B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 75.2%; Score 469; DB 2; Length 255;
Best Local Similarity 77.0%; Pred. No. 1.2e-40;
Matches 94; Conservative 7; Mismatches 17; Indels 4; Gaps 2;

QY 1 EVTLVESGDFVKPGSLKVSAAAGFAFHYAMSWVRQTPAKRLEWVAYISSGSGTY 60
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLQQSGDLVKPGSLKVSAAAGFTTFSSYGMWVRQTPDKRLEWATITSGSGTY 60
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLTGY--FDSWGQQTTL 117
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYICAR-HINRYDGAFDYWGQQTTL 119
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 118 SS 119
   |||
Db 120 SS 121
   |||

RESULT 2
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Director MGC Project;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
FT NON TER 1
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 75.1%; Score 468.5; DB 2; Length 487;
Best Local Similarity 75.0%; Pred. No. 2.7e-40;
Matches 93; Conservative 7; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVTLVESGDFVKPGSLKVSAAAGFAFHYAMSWVRQTPAKRLEWVAYISSGSGTY 60
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 EVQLVESGGLVKPGSLKLSAAAGFTTFSSYAMWVRQTPKRLWATISDGGSYTY 79
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLTGY----PDSWGQQTTL 115
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 PDNVKGRFTISRDNKNTLYLQMSHLKSEDTAMYICARDMGSPYGGYSRFDYWGQGTI 139
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 116 TVSS 119
   ||||
Db 140 TVSS 143
   ||||

RESULT 3
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
   (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -.
DR PIR; C25913; C25913.
DR HSSP; P01783; 1IGC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;
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Query Match      74.2%; Score 463; DB 2; Length 119;
Best Local Similarity 77.7%; Pred. No. 2.1e-40;
Matches 94; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

QY 1 EVTLVESGGDFVKPGSLKVCASGAFASHYAMSWVROTPAKRLEWVAIISGGSGTTY 60
Db 1 EVQLVESGGLVFPKPGSLKVCASGFTFSSYGMVSWVROTPDKRLEWVAIISGGSYTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
Db 61 PDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118

QY 119 S 119
Db 119 A 119

RESULT 4
ID Q91207 PRELIMINARY; PRT; 486 AA.
AC Q91207;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 486 AA; 52681 MW; 4FEF83152DA870B CRC64;

Query Match      72.9%; Score 455; DB 2; Length 486;
Best Local Similarity 71.0%; Pred. No. 6.9e-39;
Matches 88; Conservative 14; Mismatches 16; Indels 6; Gaps 2;

QY 1 EVTLVESGGDFVKPGSLKVCASGAFASHYAMSWVROTPAKRLEWVAIISGGSGTTY 60
Db 1 EVQLVESGGLVFPKPGSLKVCASGFTFSSYGMVSWVROTPDKRLEWVAIISGGSYTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
Db 61 PDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118

QY 119 S 119
Db 119 A 119

RESULT 5
ID Q91WP5 PRELIMINARY; PRT; 479 AA.
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match      72.1%; Score 450; DB 2; Length 479;
Best Local Similarity 73.9%; Pred. No. 2.2e-38;
Matches 88; Conservative 9; Mismatches 18; Indels 4; Gaps 1;

QY 1 EVTLVESGGDFVKPGSLKVCASGAFASHYAMSWVROTPAKRLEWVAIISGGSGTTY 60
Db 20 EVQLVESGGLVFPKPGSLKVCASGFTFSSYGMVSWVROTPDKRLEWVAIISGGNTTY 79

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 119
Db 80 SUTMKGRTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 134

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RESULT 6
Q91Z05
ID Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanches A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC010327; RAH10327.1; -.
DR STRAUSBERG R.;
DR EMBL; BC010327; RAH10327.1; -.
DR PIR; S68213; S68213.
DR HSSP; P01783; 11GC.
DR MGD; MGI:2144967; AU044919.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 70.4%; Score 439.5; DB 2; Length 473;
Best Local Similarity 72.3%; Pred. No. 2.8e-37; Indels 1; Gaps 1;
Matches 86; Conservative 10; Mismatches 22;

QY 1 EYTLVESGGDFVKPGSKLVSCAASGFAFSHYAMSWVRQTPAKRLWYAYISSGGSGTY 60
DB 20 EVQLVESGGGLVKPGSKRLSCAASGFTFSDYGMHWVRQAPKGLWYAYINSGSTIY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDSWGQGTTLTVSS 119
DB 80 ADTVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDSWGQGTTLTVSS 137

RESULT 7
Q6GMY2
ID Q6GMY2 PRELIMINARY; PRT; 606 AA.
AC Q6GMY2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

RESULT 8
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanches A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114B4C55 CRC64;

Query Match 69.2%; Score 431.5; DB 2; Length 606;
Best Local Similarity 64.2%; Pred. No. 2.5e-36;
Matches 86; Conservative 13; Mismatches 20; Indels 15; Gaps 2;

QY 1 EYTLVESGGDFVKPGSKLVSCAASGFAFSHYAMSWVRQTPAKRLWYAYISSGGSGTY 60
DB 20 QVQLVESGGGLVKPGSKLVSCAASGFTFSDYGMHWVRQAPKGLWYAYINSGSTIY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDSWGQGTTLTVSS 106
DB 80 ADSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDSWGQGTTLTVSS 139
QY 107 -DSWGQGTTLTVSS 119
DB 140 MDVWGQGTTLTVSS 153

RESULT 8
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
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15-JUL-1999 (Rel. 38, Last annotation update)
 Ig heavy chain V region 345 precursor.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=BALB/cJ;
 MEDLINE=89279149; PubMed=2499654;
 Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response";
 J. Exp. Med. 169:2007-2019 (1989).
 -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
 PIR; JT0502; HVMS34.
 DR HSSP; P01783; IIGC.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 Ig heavy chain V region 345.
 FT DOMAIN 20 49 Framework-1.
 FT DOMAIN 50 54 Complementarity-determining-1.
 FT DOMAIN 55 68 Framework-2.
 FT DOMAIN 69 85 Complementarity-determining-2.
 FT DOMAIN 86 117 Framework-3.
 FT DISULFID 41 115 By similarity.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12902 MW; 4938084627ACA99A CRC64;
 Query Match 69.1%; Score 431; DB 1; Length 117;
 Best Local Similarity 83.7%; Pred. No. 4.5e-37;
 Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSVWVQTPAKRLEWVAYISSGGSTYY 60
 DB 20 EVQLVESGGLVKPGGSLKLSAAAGFAFSSVDSNVWVQTPKRLWVAYISSGGSTYY 79
 QY 61 SSIVKGRFTISRDNKNTLYLQMSLRSEDSAMYPCTTR 98
 DB 80 PQTAKGRFTISRDNKNTLYLQMSLRSEDSAMYPCTTR 117
 RESULT 9
 Q9UL71
 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
 AC Q9UL71;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035043; AAD56279.1; -;
 DR HSSP; P01852; INFD.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 Ig heavy chain V region 345 precursor.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=BALB/cJ;
 MEDLINE=89279149; PubMed=2499654;
 Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response";
 J. Exp. Med. 169:2007-2019 (1989).
 -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
 PIR; JT0502; HVMS34.
 DR HSSP; P01783; IIGC.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 Ig heavy chain V region 345.
 FT DOMAIN 20 49 Framework-1.
 FT DOMAIN 50 54 Complementarity-determining-1.
 FT DOMAIN 55 68 Framework-2.
 FT DOMAIN 69 85 Complementarity-determining-2.
 FT DOMAIN 86 117 Framework-3.
 FT DISULFID 41 115 By similarity.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12902 MW; 4938084627ACA99A CRC64;
 Query Match 69.1%; Score 431; DB 1; Length 117;
 Best Local Similarity 83.7%; Pred. No. 4.5e-37;
 Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSVWVQTPAKRLEWVAYISSGGSTYY 60
 DB 20 EVQLVESGGLVKPGGSLKLSAAAGFAFSSVDSNVWVQTPKRLWVAYISSGGSTYY 79
 QY 61 SSIVKGRFTISRDNKNTLYLQMSLRSEDSAMYPCTTR 98
 DB 80 PQTAKGRFTISRDNKNTLYLQMSLRSEDSAMYPCTTR 117
 RESULT 9
 Q9UL71
 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
 AC Q9UL71;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035043; AAD56279.1; -;
 DR HSSP; P01852; INFD.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.

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Query Match      68.8%; Score 429; DB 2; Length 480;
Best Local Similarity 70.8%; Pred. No. 3.5e-36;
Matches 85; Conservative 13; Mismatches 18; Indels 4; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 DVKLVESGGGLVKPGGSLKLSCAAGSFIFSNYSMSVVRQTPKRLWATISNSGYATHY 78
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTY-YFDSWGGGTTLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 PDSMKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTY-YFDSWGGGTTLTVSS 135
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q55ZL8 PRELIMINARY; PRT; 196 AA.
AC Q65ZL8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE VH7183-DSP2-JH3-CHI protein (Fragment)
GN Name=VH7183-DSP2-JH3-CHI;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95362300; PubMed=7635518;
RA Komori T., Sugiyama H.;
RT "An aberrant splicing using a 3' cryptic splice site within the CHI
RL exon induces truncated mu-chain production.";
DR EMBL; S79401; AAB35023.2; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 196
SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match      68.3%; Score 426; DB 2; Length 196;
Best Local Similarity 86.5%; Pred. No. 2.7e-36;
Matches 83; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EYMLVESGGGLVKPGGSLKLSCAAGSFIFSNYSMSVVRQTPKRLWATISNSGGSYTY 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFC 96
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFC 115
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q6P181 PRELIMINARY; PRT; 478 AA.
AC Q6P181;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match      68.3%; Score 426; DB 2; Length 478;
Best Local Similarity 66.7%; Pred. No. 7.1e-36;
Matches 86; Conservative 10; Mismatches 23; Indels 10; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVANIKQDGEKY 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR-----VKLGTYF--DSWG 110
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 VDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR-----VKLGTYF--DSWG 139
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 111 QGTTLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 KGTIVTVSS 148
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CA245931.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003106; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 68.1%; Score 425; DB 2; Length 464;
Best Local Similarity 70.0%; Pred. No. 8.8e-36;
Matches 84; Conservative 14; Mismatches 20; Indels 2; Gaps 2;

QY 1 EVTLVSGDGFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLLEWVAYISS-GGSGTY 59
DB 20 EVQLVESGGGLVPPGGSRLSLCAASGFTFSYSMMWVRQAPGKLEWVSFSSRGGSY 79
QY 60 YSDSVKGRFTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVSS 119
DB 80 YADSVKGRFTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVSS 138

RESULT 14
Q6PDB8 PRELIMINARY; PRT; 485 AA.
AC Q6PDB8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S.C., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058814; AAH58814.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003106; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

Query Match 67.9%; Score 424; DB 2; Length 485;
Best Local Similarity 67.8%; Pred. No. 1.2e-35;
Matches 82; Conservative 12; Mismatches 25; Indels 2; Gaps 1;

QY 1 EVTLVSGDGFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLLEWVAYISSGGSGTY 60
DB 20 DVQLVESGGGLVPPGGSRLSLCAASGFTFSNYGMHWVRQAPKLEWVAYISSSGTIFY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
DB 80 ADTVKGRFTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 139
QY 119 S 119
DB 140 S 140

RESULT 15
HV16 MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adegugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; J00522; AAD15290.1; -.
DR PIR; E90809; G1MS21.
```

DR PDB: 1IGC; X-ray; H=-
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136 Ig heavy chain V region MOPC 21.
FT DOMAIN 115 119 D segment.
FT DOMAIN 120 136 JH4 segment.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (in Ref. 2).
FT CONFLICT 89 90 DN -> ND (in Ref. 2).
FT CONFLICT 115 115 W -> H (in Ref. 2).
FT CONFLICT 120 120 Y -> W (in Ref. 2).
FT STRAND 19 23
FT STRAND 26 28
FT TURN 30 31
FT STRAND 34 41
FT HELIX 45 47
FT STRAND 50 55
FT STRAND 61 67
FT TURN 69 70
FT STRAND 74 76
FT HELIX 78 80
FT STRAND 81 81
FT TURN 82 83
FT STRAND 84 89
FT TURN 90 93
FT STRAND 94 99
FT HELIX 104 106
FT STRAND 108 114
FT TURN 118 119
FT STRAND 125 126
FT STRAND 130 134
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 2276A98DBDBF7016 CRC64;

Query Match 67.9%; Score 423.5; DB 1; Length 136;
Best Local Similarity 69.2%; Pred. No. 3'2e-36;
Matches 83; Conservative 12; Mismatches 24; Indels 1; Gaps 1;
Qy 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60
Db 17 DVQLVESGGGLVPGGSRKLSAAAGFTFSFGMEHWVRQAPKLEWVAYISSGGSTLHY 76
Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYECTRVKLGTY-FDSWGGQTTLTVSS 119
Db 77 ADTVKGRFTISRDNKNTLYLQMTSLRSEDTAMYCYARWGNYPYAMDYWGQGSTVTSS 136

Search completed: August 1, 2005, 09:17:10
Job time : 31.8793 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 32.5277 Seconds
(without alignments)
1284.140 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIQMTQTASLPASLGRVLT.....HQYSKLPWTFGGTKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	100.0	108	4	AAB81990
2	572	100.0	108	6	ABU11013
3	572	100.0	128	3	AAB01628
4	572	100.0	128	4	AAB81978
5	572	100.0	128	6	ABU11003
6	564	98.6	128	2	AAZ28368
7	562	98.3	128	2	AAR33257
8	557	97.4	128	2	AAR53340
9	521	91.1	108	2	AAW00834
10	520	90.9	127	2	AAR12359
11	516	90.2	108	2	AAW04177
12	516	90.2	108	2	AAW16620
13	516	90.2	128	4	AAB81998
14	516	90.2	650	6	ABR62591
15	516	90.2	651	6	ABR62590
16	515	90.0	126	2	AAR12237
17	514	89.9	108	4	AAB81988
18	514	89.9	128	4	AAB81999
19	511	89.3	128	4	AAB81992
20	510	89.2	108	2	AAW70620
21	510	89.2	108	5	ABP61189
22	508	88.8	108	6	ABU11011
23	507	88.6	128	4	AAB81994
24	507	88.6	214	8	ADN41870
25	506	88.5	128	4	AAB81995

131	87.8	502	26	AAR84553	Aar84553 MAb SCH94
128	87.6	501	27	AAB81997	Aab81997 Ganglios
131	87.4	500	28	AD126634	Ad126634 Human ant
128	87.2	499	29	AAB81996	Aab81996 Ganglios
112	87.1	498	30	AAE00697	Aae00697 Human imm
109	86.9	497	31	AAB82050	Aab82050 Mouse mon
109	86.9	497	32	ABP72768	Abp72768 Anti-Full
128	86.9	497	33	AAB81993	Aab81993 Ganglios
119	86.5	495	34	ADM78045	Adm78045 Human SKB
107	86.4	494	35	ADQ09630	Adq09630 Variable
108	86.4	494	36	AAB81986	Aab81986 Ganglios
107	85.8	491	37	ABU18571	Abj18571 Ganglios
107	85.8	491	38	ABU18574	Abj18574 Ganglios
107	85.7	490	39	AAW66098	Aaw66098 anti-CD22
107	85.7	490	40	AAO27199	Aao27199 Murine an
107	85.7	490	41	ADC84579	Adc84579 CDR3 heav
107	85.7	490	42	ADH50840	Adh50840 Mouse ant
109	85.7	490	43	ADG25821	Adg25821 Anti-CD30
107	85.3	488	44	AAW49812	Aaw49812 Amino aci
107	85.3	488	45	ABR55867	Abr55867 Anti-glyc
107	85.3	488	46	ADN49724	Adn49724 Variable
108	85.3	488	47	AAZ94216	Aaz94216 Murine co
127	85.3	488	48	AAR39265	Aar39265 Mouse C4G
127	85.3	488	49	AAW11815	Aaw11815 Mouse ant
127	85.3	488	50	AAW60033	Aaw60033 Mouse ant
127	85.3	488	51	AAW49809	Aaw49809 Variable
127	85.3	488	52	AAW19871	Aaw19871 Activatin
555	85.3	488	53	AAB19873	Aab19873 Activatin
565	85.3	488	54	AAB19872	Aab19872 Activatin
601	85.3	488	55	AAO7461	Aao7461 An immuno
601	85.3	488	56	ABG72265	Abg72265 Recombina
637	85.3	488	57	AAU75365	Aau75365 Diptheri
637	85.3	488	58	AAU75370	Aau75370 Diptheri
642	85.3	488	59	AAU75382	Aau75382 Diptheri
642	85.3	488	60	AAO29675	Aao29675 Anti-T ce
643	85.3	488	61	AAU75390	Aau75390 Diptheri
643	85.3	488	62	AAO29670	Aao29670 Anti-T ce
656	85.3	488	63	AAU75383	Aau75383 Immunotox
657	85.3	488	64	AAU75389	Aau75389 Diptheri
704	85.3	488	65	AAB19888	Aab19888 M1V envel
108	85.1	487	66	AAV71445	Aay71445 Murine mo
108	85.1	487	67	AAZ56704	Aay56704 Murine an
108	85.1	487	68	ABO10815	Abo10815 Mouse mon
302	85.1	487	69	ABR60206	Abr60206 Bispecifi
504	85.1	487	70	ADD25787	Add25787 Binding d
555	85.1	487	71	ADB86039	Adb86039 Anti-CD3
555	85.1	487	72	ADK00036	Adk00036 Chimeric
555	85.1	487	73	ABF59985	Abf59985 Antibody
107	84.8	485	74	ADF69648	Adf69648 Humanised
107	84.6	484	75	AAO23067	Aao23067 Murine K8
109	84.6	484	76	AAR52039	Aar52039 Light cha
127	84.6	484	77	AAO23066	Aao23066 Murine K8
127	84.6	484	78	ABR62342	Abr62342 Anti-HLA-
107	84.4	483	79	AAR30768	Aar30768 Murine an
652	84.4	483	80	AAU75448	Aau75448 Immunotox
895	84.4	483	81	AAU75369	Aau75369 Diptheri
895	84.4	483	82	AAU75368	Aau75368 Diptheri
895	84.4	483	83	AAU75374	Aau75374 Diptheri
895	84.4	483	84	AAO29673	Aao29673 Anti-T ce
896	84.4	483	85	AAU75367	Aau75367 Diptheri
896	84.4	483	86	AAU75366	Aau75366 Diptheri
896	84.4	483	87	AAU75373	Aau75373 Diptheri
896	84.4	483	88	AAO29672	Aao29672 Anti-T ce
896	84.4	483	89	AAO29671	Aao29671 Anti-T ce
896	84.4	483	90	AAO29676	Aao29676 Anti-T ce
899	84.4	483	91	AAU75375	Aau75375 Diptheri
899	84.4	483	92	AAO29674	Aao29674 Anti-T ce
107	84.0	480	93	ADN49402	Adn49402 Murine an
215	83.8	479	94	AD019050	Ado19050 Murine an
247	83.7	479	95	ADK42701	Adk42701 14B7 scFv
107	83.4	477	96	ABO10814	Abo10814 Mouse mon
127	83.0	475	97	AAR32121	Aar32121 Anti-CD4
127	82.9	474	98	AAR28670	Aar28670 pPM-K3 pr

99 474 82.9 667 6 ABP97414 Anti-huma
100 473 82.7 127 2 AAR29010 p146-k3 p

ALIGNMENTS

RESULT 1

AAB81990 ID AAB81990 standard; protein; 108 AA.

AC AAB81990;

DT 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.

XX Mus musculus.

OS WO200123432-A1.

PN PD

XX 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PA Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

XX Claim 11; Page 174-175; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 572; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.4e-39;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60

DB 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60

QY 61 RPSGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108

DB 61 RPSGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108

RESULT 2

ABU11013 ID ABU11013 standard; protein; 108 AA.

XX AC ABU11013;

XX 04-FEB-2003 (first entry)

DT 04-FEB-2003 (first entry)

XX

DE Modified ganglioside GD3 antibody associated protein #6.
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

PN WO200278739-A1.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 7; Page 113; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 572; DB 6; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.4e-39;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60

DB 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60

QY 61 RPSGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108

DB 61 RPSGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108

RESULT 3

AAB01628

ID AAB01628 standard; protein; 128 AA.

XX AC AAB01628;

DT 07-DEC-2000 (first entry)

XX Murine immunoglobulin light chain variable region.

XX Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
KW humanised antibody.

XX Mus sp.

XX Key Location/Qualifiers

XX Peptide 1..20

XX Protein /label= signal_peptide

XX /label= mature_immunoglobulin_light_chain_v_region

XX EP1013761-A2.


```

XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 1; Page 140; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX SQ Sequence 128 AA;
XX
XX Query Match 100.0%; Score 572; DB 4; Length 128;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-39;
XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 DIQMTQTASSLPASLGRVITSCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
XX |||||||
Db 21 DIQMTQTASSLPASLGRVITSCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80
XX |||||||
Qy 61 RPSGGSGTDYSLTISNLPEDIATYFCHOYSKLPWTFGGGTKLEIKR 108
XX |||||||
Db 81 RPSGGSGTDYSLTISNLPEDIATYFCHOYSKLPWTFGGGTKLEIKR 128
XX |||||||
XX
XX RESULT 5
XX ABU11003
XX ID ABU11003 standard; protein; 128 AA.
XX AC ABU11003;
XX
XX DT 04-FEB-2003 (first entry)
XX
XX DE Modified ganglioside GD3 antibody associated protein #2.
XX
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX OS Mus musculus.
XX
XX XN WO200278739-A1.
XX
XX PD 10-OCT-2002.
XX
XX PF 29-MAR-2002; 2002WO-JP003170.
XX
XX PR 29-MAR-2001; 2001JP-00097483.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Example 3; Page 98; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX SQ Sequence 128 AA;

```

PD 28-JUN-2000.

XX
PT New human type complementation-determining region-transplanted antibody
PF and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
PR activity in cancer.
XX
PS Example 1; Page 140; 183pp; Japanese.
XX

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 108
DB 81 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 128

RESULT 4
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KM Mus musculus.
XX
OS WO200123432-A1.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PP 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 108
DB 81 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 128

RESULT 5
ABU11003
ID ABU11003 standard; protein; 128 AA.
XX
AC ABU11003;
XX
DT 04-FEB-2003 (first entry)
DE Modified ganglioside GD3 antibody associated protein #2.
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX Mus musculus.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-JP003170.
XX
PR 29-MAR-2001; 2001JP-00097483.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX
XX WPI; 2003-067410/06.
XX
PT Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
PS Example 3; Page 98; 121pp; Japanese.
XX

CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 108
DB 81 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 128

RESULT 4
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KM Mus musculus.
XX
OS WO200123432-A1.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PP 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 108
DB 81 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 128

RESULT 4
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KM Mus musculus.
XX
OS WO200123432-A1.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PP 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 108
DB 81 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 128

RESULT 4
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KM Mus musculus.
XX
OS WO200123432-A1.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PP 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 108
DB 81 RFSGGSGSDYSLTISNLEPEDIAITYFCHQYSKLPTWTFGGGTGLEIKR 128

RESULT 4
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KM Mus musculus.
XX
OS WO200123432-A1.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PP 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQKDPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQQ

```
Query Match      100.0%; Score 572; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
   |||||

QY 61 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 108
   |||||
Db 81 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 128
   |||||

RESULT 6
AA28368
ID AA28368 standard; protein; 128 AA.
XX
AC AA28368;
XX
DT 04-NOV-1999 (first entry)
XX
DE pKM641 LA2 immunoglobulin light chain.
XX
KW antibody; nucleotide; genomic; hypervariable region; chimeric;
KW light chain; amino acid.
XX
OS Mus sp.
XX
PN US5939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX
DR WPI; 1999-468416/39.
XX
DR N-PSDB; AA299481.
XX
PT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641LA2, A methionine
CC codon, presumably the initiation codon ATG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer,
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The
CC chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal antibodies
XX
SQ Sequence 128 AA;

Query Match      98.6%; Score 564; DB 2; Length 128;
Best Local Similarity 99.1%; Pred. No. 1.8e-38;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
   |||||

QY 61 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 108
   |||||
Db 81 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 128
   |||||

Query Match      98.3%; Score 562; DB 2; Length 128;
Best Local Similarity 99.1%; Pred. No. 2.7e-38;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
   |||||

QY 61 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 108
   |||||
Db 81 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 128
   |||||

RESULT 7
AAR33257
ID AAR33257 standard; protein; 128 AA.
XX
AC AAR33257;
XX
DT 25-MAR-2003 (revised)
DT 12-JUL-1993 (first entry)
XX
DE Rat immunoglobulin L chain variable region of pKM641LA2.
XX
KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
KW humanised; chimeric; antibody; expression vector.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /note= "Signal peptide"
FT Protein 21..128
FT Protein /note= "Mature protein"
XX
PN EP533199-A2.
XX
PD 24-MAR-1993.
XX
PF 18-SEP-1992; 92EP-00116026.
XX
PR 18-SEP-1991; 91JP-00238375.
XX
PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX
PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
DR WPI; 1993-095510/12.
XX
DR N-PSDB; AAQ33258.
XX
PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
PT cancers, such as melanoma, neuroblastoma, etc.
XX
PS Claim 6; Page 30-31; 63pp; English.
XX
CC The sequences given in AAR33256-57 represent rat heavy and light chain
CC variable regions respectively. The DNA sequences encoding these proteins
CC were used in the construction of humanised chimeric antibody expression
CC vectors. In these humanised antibodies none of the amino acids of the non
CC -human animal Ab variable region have been changed. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 128 AA;

Query Match      98.3%; Score 562; DB 2; Length 128;
Best Local Similarity 99.1%; Pred. No. 2.7e-38;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
   |||||

QY 61 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 108
   |||||
Db 81 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 128
   |||||

RESULT 8
AAR53340
ID AAR53340 standard; protein; 128 AA.
XX
AC AAR53340;
XX
DT 18-NOV-1994 (first entry)
XX
DE KM641 H chain variable region.
```

XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
 KW expression vector; heavy; light; chain; hypervariable region; CDR;
 KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= sig_peptide
 XX AU9346181-A.
 XX 17-MAR-1994.
 XX 07-SEP-1993; 93AU-00046181.
 XX 07-SEP-1992; 92JP-00238452.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
 XX WPI; 1994-126857/16.
 XX N-PSDB; AAQ45438.
 XX Humanised antibody specific for ganglioside GM2 - used for producing a
 PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
 XX Example 2; Page 115-116; 191pp; English.
 XX Example 2 describes the construction of the vector pCh1641HA1 for
 CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
 CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
 CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
 CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
 CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
 CC was constructed by joining the H chain variable region gene from
 CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
 CC synthetic DNAs given in AAQ63439 and AAQ63440
 XX Sequence 128 AA;
 SQ
 Query Match 97.4%; Score 557; DB 2; Length 128;
 Best Local Similarity 98.1%; Pred. No. 6.8e-38;
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
 DB 21 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
 QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTVKLEIKR 108
 DB 81 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTVKLEIKR 128
 RESULT 9
 AAW00834
 ID AAW00834 standard; protein; 108 AA.
 AC AAW00834;
 XX 20-MAY-1997 (first entry)
 DE Variable light chain of anti-human Fas ligand antibody NOK-1.
 XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
 KW NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
 KW hepatitis; infectious mononucleosis; systemic lupus erythematosus.
 XX Mus musculus.
 XX W09629350-A1.
 PN

XX 26-SBP-1996.
 XX 21-MAR-1996; 96WO-JP000734.
 XX 20-MAR-1995; 95JP-00087420.
 XX 27-OCT-1995; 95JP-00303492.
 XX (SUME) SUMITOMO ELECTRIC IND CO.
 XX Kayagaki N, Yagita H, Okumura K, Nakata M;
 XX WPI; 1996-443140/44.
 XX N-PSDB; AAT39560.
 XX Monoclonal antibody specifically recognising the Fas ligand - useful for
 PT the detection of Fas ligands either on cell surface or in solution.
 XX Claim 41; Page 93-94; 133pp; Japanese.
 XX The present sequence is the light chain variable region of the anti-human
 CC Fas ligand monoclonal antibody (Mab) NOK-1. NOK-1 is produced by the
 CC hybridoma NOK-1 (PERM BP-5044), which was prepared by immunising mice
 CC with transformed human Fas ligand expressing COS cells, and fusing spleen
 CC cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
 CC cells. The Mab recognises the human Fas ligand on the cell surface or in
 CC solution, and can be used to inhibit the apoptosis inducing cell surface
 CC Fas ligand/Fas reaction. The Mab can also be used for a Fas ligand assay
 CC in biological samples (e.g. human blood), especially for disease
 CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
 CC erythematosus
 XX Sequence 108 AA;
 SQ
 Query Match 91.1%; Score 521; DB 2; Length 108;
 Best Local Similarity 90.7%; Pred. No. 4.9e-35;
 Matches 98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
 DB 1 DIQMTQTSSLSASLGRVITSCASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60
 QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTVKLEIKR 108
 DB 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSEFPWTFGGTVKLEIKR 108
 RESULT 10
 AAR12359
 ID AAR12359 standard; protein; 127 AA.
 XX AAR12359;
 AC AAR12359;
 XX 25-MAR-2003 (revised)
 DT 15-AUG-1991 (first entry)
 XX Light (kappa) chain variable region of murine 1C11 immunoglobulin.
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
 XX Mus musculus.
 XX W09107493-A.
 XX 30-MAY-1991.
 XX 13-NOV-1989; 89US-00433730.
 XX 13-NOV-1989; 89US-00433730.
 XX (XOMA) XOMA CORP.
 XX (GEC) GREEN CROSS CORP.
 XX

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PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX WPI; 1991-178105/24.
DR N-PSDB; AAQ12061.
XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX Disclosure; Fig 13; 107pp; English.
XX This is the light (kappa)- chain variable (V) region of a mouse
CC monoclonal antibody (MAB), 1C11, and is specific for an HIV-1 viral
CC antigen. It is used in the construction of a chimeric MAB comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric MABs are more effective than murine MAB 1C11 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric MABs can be
CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC 60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to
CC correct DR field.)
XX Sequence 127 AA;
SQ
Query Match 90.9%; Score 520; DB 2; Length 127;
Best Local Similarity 91.6%; Pred. No. 7e-35;
Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQKPDGTVKLLIYTSLSHSGVPS 80
QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107
DB 81 RFSGGSGTDYSLTISNLEPEDIATYCYQYSKLPWTFGGKLEIK 127
RESULT 11
AAW04177
ID AAW04177 standard; protein; 108 AA.
AC AAW04177;
XX
XX 19-MAY-1997 (first entry)
XX Variant variable light chain of Fas ligand antibody NOK-1.
DE
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
KW NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
KW hepatitis; infectious mononucleosis; systemic lupus erythematosus;
KW variant.
XX
XX Mus musculus.
XX
XX WO9629350-A1.
PN
XX 26-SEP-1996.
PD
XX 21-MAR-1996; 96WO-JP000734.
PF
XX 20-MAR-1995; 95JP-00087420.
PR 27-OCT-1995; 95JP-00303492.
XX (SUME ) SUMITOMO ELECTRIC IND CO.
PA
XX Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
DR N-PSDB; AAT39550.
XX Monoclonal antibody specifically recognising the Fas ligand - useful for
PT

```

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PT the detection of Fas ligands either on cell surface or in solution.
XX Claim 20; Page 80-81; 133pp; Japanese.
PS
XX The present sequence is a variant light chain variable region of the anti
CC -human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by
CC the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
CC with transformed human Fas ligand expressing COS cells, and fusing spleen
CC cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
CC cells. The MAB recognises the human Fas ligand on the cell surface or in
CC solution, and can be used to inhibit the apoptosis inducing cell surface
CC Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay
CC in biological samples (e.g. human blood), especially for disease
CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
CC erythematosus
XX
XX Sequence 108 AA;
SQ
Query Match 90.2%; Score 516; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.3e-34;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60
QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCQYSEFPWTFGGGKLEIKR 108
RESULT 12
AAW16620
ID AAW16620 standard; protein; 108 AA.
XX
XX AAW16620;
XX
XX 14-JAN-1998 (first entry)
XX
XX Anti-human FasL antibody (NOK1) light chain variable region.
DE
XX Light chain; variable region; mouse; murine; human; Fas ligand; FasL;
KW monoclonal antibody; MAB; hybridoma; treatment; hepatitis;
KW hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell;
KW glutamate oxaloacetate; pyruvate transaminase.
XX
XX Mus sp.
XX
XX WO9715326-A1.
PN
XX 01-MAY-1997.
PD
XX 24-OCT-1996; 96WO-JP003089.
PF
XX 27-OCT-1995; 95JP-00303491.
PR (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX Seino K, Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1997-258767/23.
DR N-PSDB; AAT66710.
XX
XX Anti-human Fas Ligand antibody to treat hepatitis - controls apoptosis in
PT liver cells and improves liver function.
XX
XX Claim 6; Page 30-31; 51pp; Japanese.
PS
XX The present sequence is the light chain variable region of the murine
CC anti-human Fas ligand (FasL) monoclonal antibody (MAB) NOK1, which is
CC expressed by the hybridoma NOK1 (FERM BP-5044). The MAB can be used in
CC the preparation of a composition for the effective oral or parenteral
CC treatment of hepatitis, including hepatitis caused by hepatitis B or C

```

CC virus. The composition controls apoptosis in liver cells caused by the
 CC binding of FasL to Fas expressing liver cells, and improves liver
 CC function by improving blood glutamate oxaloacetate and pyruvate
 CC transaminase levels. The composition is given in a dosage of 0.0001-1000,
 CC preferably 0.01-600 mg/day. Spleen cells from mice immunised with FasL
 CC expressing COS cells were fused with mouse myeloma cells to produce
 CC hybridomas. The hybridomas were screened for anti-FasL activity, and the
 CC active clones NOK1-5 isolated
 XX
 SQ Sequence 108 AA;

Query Match 90.2%; Score 516; DB 2; Length 108;
 Best Local Similarity 89.8%; Pred. No. 1.3e-34;
 Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DIQMTQTASSLPASLGRVITISCSASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 60
 DB 1 DIQMTQSPSSLSASLGRVITISCSASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 60
 QY 61 RFGSGSGTDYSLTISNLEPEDATYFCQYKSLPMTFGGTTKLEIKR 108
 DB 61 RFGSGSGTDYSLTISNLEPEDATYFCQYKSLPMTFGGTTKLEIKR 108

RESULT 13
 AAB81998
 ID AAB81998 standard; protein; 128 AA.
 AC AAB81998;
 DT 03-JUL-2001 (first entry)
 DE Ganglioside GD3 specific antibody related protein #7.
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KW Cancer.
 OS Synthetic.
 XX WO200123432-A1.
 XX 05-APR-2001.
 XX 29-SEP-2000; 2000WO-JP006774.
 XX 30-SEP-1999; 99JP-00278291.
 XX 06-APR-2000; 2000JP-00105088.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266143/27.
 XX N-PSDB; AAF86912.

New human type complementation-determining region-transplanted antibody
 and derivatives against ganglioside GD3, useful in diagnosis and therapy
 of e.g. tumors, with low antigenicity, little side effects but potent
 activity in cancer.
 XX Example 3; Page 164-165; 183pp; Japanese.
 XX The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 XX Sequence 128 AA;

Query Match 90.2%; Score 516; DB 4; Length 128;
 Best Local Similarity 88.9%; Pred. No. 1.5e-34;
 Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIQMTQTASSLPASLGRVITISCSASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 60
 DB 1 DIQMTQSPSSLSASLGRVITISCSASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 60
 QY 61 RFGSGSGTDYSLTISNLEPEDATYFCQYKSLPMTFGGTTKLEIKR 108
 DB 61 RFGSGSGTDYSLTISNLEPEDATYFCQYKSLPMTFGGTTKLEIKR 108

QY 1 DIQMTQTASSLPASLGRVITISCSASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 60
 DB 21 DIQMTQSPSSLSASLGRVITISCSASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 80
 QY 61 RFGSGSGTDYSLTISNLEPEDATYFCQYKSLPMTFGGTTKLEIKR 108
 DB 81 RFGSGSGTDYSLTISNLEPEDATYFCQYKSLPMTFGGTTKLEIKR 128

RESULT 14
 ABR62591
 ID ABR62591 standard; protein; 650 AA.
 AC ABR62591;
 DT 06-NOV-2003 (first entry)
 DE Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein.
 KW CD7; antibody; TH-69; scFv; exotoxin A; immunotoxin; cytostatic;
 KW immunosuppressive; vaccine.
 XX Mus sp.
 OS Pseudomonas sp.
 OS Synthetic.
 OS Chimeric.

PH Key Location/Qualifiers
 FT Region 7..265.
 FT /label= scFv
 FT Region 125..285
 FT /label= Linker
 FT Region 286..645
 FT /label= ETA
 XX WO2003051926-A2.
 XX 26-JUN-2003.
 XX 11-DEC-2002; 2002WO-EP014064.
 XX 14-DEC-2001; 2001US-0339422P.
 XX (UYER-) UNIV ERLANGEN-NURNBERG.
 XX Fey GHM, Gramatzki M, Peipp M;
 XX WPI; 2003-523519/49.
 XX N-PSDB; ACP05482.

New fusion protein comprising functionally linked components of an anti-
 CD7 antibody or its fragment and an immunotoxin, useful for treating CD7
 positive acute T-cell and/or myeloid leukemias, or Graft-versus-host
 disease.
 XX Claim 9; Page 8; 55pp; English.

The present sequence is that of a novel fusion protein comprising an scFv
 fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of
 Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including
 an N-terminal 6xHis tag and C-terminal KDEL sequence. This novel fusion
 protein binds to CD7-positive T-lymphoid cells and kills them by the
 induction of apoptosis. It is an example of anti-CD7 scFv immunotoxin
 fusion proteins of the invention. An expression vector, host cells, a
 method for producing the fusion protein, and a vaccine comprising the
 fusion protein are claimed. The fusion protein is used in the treatment
 of disorders involving a hyperproliferation of CD7-positive cells,
 especially acute T-cell and/or myeloid leukemia, and also in the
 treatment or prophylaxis of Graft-versus-host disease. A claimed method
 of conditioning an animal (e.g. a human) to be transplanted with donor
 cells, tissue or organ comprises: (a) depleting the CD7-bearing cell
 population in the animal; (b) providing a transplant comprising isolated

CC bone marrow and/or stem cell-enriched peripheral blood cells of the
CC donor, where the CD7-bearing cell population in (a) and/or the transplant
CC in (b) are treated with a T-cell depleting effective amount of the fusion
CC protein or therapeutic composition comprising the fusion protein; and (c)
CC introducing the transplant into the animal

XX Sequence 650 AA;

Query Match 90.2%; Score 516; DB 6; Length 650;
Best Local Similarity 90.7%; Pred. No. 7.5e-34;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60

DB 17 DIQMTQTSSLSASLGDRTVITSCSASQGISNYLNWYQKPDGTVKLLIYTSLSHSGVPS 76

QY 61 RFSGGSGTDYSLTISNLEPEDYATYFCHQYKSLPWTFFGGTKLEIKR 108

DB 77 RFSGGSGTDYSLTISNLEPEDYATYFCHQYKSLPWTFFGGTKLEIKR 124

RESULT 15

ABR62590

ID ABR62590 standard; protein; 651 AA.

XX ABR62590;

XX 06-NOV-2003 (first entry)

DE Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein.

XX CD7; antibody; TH-69; scFv; exotoxin A; immunotoxin; cytostatic;

KW immunosuppressive; vaccine.

XX Mus sp.

OS Pseudomonas sp.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

FT Region 7..265

FT /label= scFv

FT Region 125..285

FT /label= Linker

FT Region 286..646

FT /label= ETA

XX WO2003051926-A2.

XX 26-JUN-2003.

XX 11-DEC-2002; 2002WO-EP014064.

XX 14-DEC-2001; 2001US-0339422P.

XX (UYER-) UNIV ERLANGEN-NUERNBURG.

XX Fey GHM, Gramatzki M, Peipp M;

XX WPI; 2003-523519/49.

XX N-PSDB; ACF05481.

XX New fusion protein comprising functionally linked components of an anti-
PT CD7 antibody or its fragment and an immunotoxin, useful for treating CD7
PT positive acute T-cell and/or myeloid leukemias, or Graft-versus-host
PT disease.
XX Claim 9; Page 7; 55pp; English.

XX The present sequence is that of a novel fusion protein comprising an scFv
CC fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of
CC Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including
CC an N-terminal 6xHis tag and C-terminal REDLK sequence. This novel fusion

CC protein binds to CD7-positive T-lymphoid cells and kills them by the
CC induction of apoptosis. It is an example of anti-CD7 scFv immunotoxin
CC fusion proteins of the invention. An expression vector, host cells, a
CC method for producing the fusion protein, and a vaccine comprising the
CC fusion protein are claimed. The fusion protein is used in the treatment
CC of disorders involving a hyperproliferation of CD7-positive cells,
CC especially acute T-cell and/or myeloid leukaemia, and also in the
CC treatment or prophylaxis of Graft-versus-host disease. A claimed method
CC of conditioning an animal (e.g. a human) to be transplanted with donor
CC cells, tissue or organ comprises: (a) depleting the CD7-bearing cell
CC population in the animal; (b) providing a transplant comprising isolated
CC bone marrow and/or stem cell-enriched peripheral blood cells of the
CC donor, where the CD7-bearing cell population in (a) and/or the transplant
CC in (b) are treated with a T-cell depleting effective amount of the fusion
CC protein or therapeutic composition comprising the fusion protein; and (c)
CC introducing the transplant into the animal

XX Sequence 651 AA;

Query Match 90.2%; Score 516; DB 6; Length 651;

Best Local Similarity 90.7%; Pred. No. 7.5e-34;

Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60

DB 17 DIQMTQTSSLSASLGDRTVITSCSASQGISNYLNWYQKPDGTVKLLIYTSLSHSGVPS 76

QY 61 RFSGGSGTDYSLTISNLEPEDYATYFCHQYKSLPWTFFGGTKLEIKR 108

DB 77 RFSGGSGTDYSLTISNLEPEDYATYFCHQYKSLPWTFFGGTKLEIKR 124

Search completed: August 1, 2005, 09:10:15

Job time : 35.5277 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 8.1913 Seconds
(without alignments)
983.287 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIQWQTASSLPASLGRVT.....HOYSKLPWTFGGTKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	572	100.0	128	4	US-09-225-322B-19
3	572	100.0	128	4	US-09-764-304-10
4	572	100.0	128	4	US-09-764-304-19
5	516	90.2	108	3	US-09-065-059-3
6	503	87.9	107	2	US-08-652-558-35
7	502	87.8	111	1	US-08-236-520-2
8	502	87.8	131	5	PCT-US95-05262-2
9	498	87.1	112	3	US-08-487-761-13
10	497	86.9	109	4	US-09-386-658A-4
11	490	85.7	108	4	US-09-232-290-21
12	488	85.3	107	1	US-08-458-516-9
13	488	85.3	127	1	US-08-458-516-5
14	488	85.3	127	3	US-08-649-100-17
15	487	85.1	108	3	US-09-199-149-7
16	487	85.1	274	4	US-09-813-659-30
17	487	85.1	274	4	US-09-549-067A-30
18	487	85.1	302	1	US-08-121-054C-18
19	487	85.1	302	1	US-08-121-054C-30
20	487	85.1	302	3	US-08-539-436-18
21	487	85.1	302	3	US-08-539-436-30
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28	483	84.4	107	3	US-08-437-642B-16
29	483	84.4	107	4	US-08-146-206C-16
30	483	84.4	107	4	US-09-705-686-16
31	483	84.4	107	4	US-09-705-392A-16
32	483	84.4	107	4	US-09-705-398-16
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54	453	79.2	491	4	US-10-011-125A-2
55	451	78.8	109	1	US-07-942-245-11
56	451	78.8	211	4	US-09-170-769A-8
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60	439.5	76.8	108	3	US-08-964-690-24
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64	437	76.4	109	4	US-09-357-707-21
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97	426	74.5	233	4	US-09-705-398-25
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ALIGNMENTS

```
RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-09-225-322B-10
Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.8e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASIGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASIGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 128

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-09-225-322B-19
Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.8e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASIGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASIGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 128

RESULT 3
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cdna KM-641
US-09-764-304-10
Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.8e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASIGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASIGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 128
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Db 81 RFSGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128

RESULT 4

US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. 6495866
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764.304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.8e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGLDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASLGLDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 81 RFSGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128

RESULT 5

US-09-065-059-3
; Sequence 3, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:
; APPLICANT: SEINO, Ken-ichiro
; APPLICANT: KAVAGAKI, No. 6068841uhiko
; APPLICANT: YAGITA, Hideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,059
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: P-42,368
; REFERENCE/DOCKET NUMBER: 50356-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-518-5100
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-065-059-3

Query Match 90.2%; Score 516; DB 3; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.6e-45;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGLDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASLGLDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60
QY 61 RFSGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 61 RFSGSGGTDYSLTISNLEPEDIATYFCQYSEFPWTFGGGTKLEIKR 108

RESULT 6

US-08-652-558-35
; Sequence 35, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:

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; ; LENGTH: 107 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
US-08-652-558-35

Query Match      87.9%; Score 503; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.5e-44;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107
Db 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107

RESULT 7
US-08-236-520-2
; Sequence 2, Application US/08236520
; Patent No. 5591629
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,520
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 27,227
; REFERENCE/DOCKET NUMBER: MMV92-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-520-2

Query Match      87.8%; Score 502; DB 1; Length 131;
Best Local Similarity 88.9%; Pred. No. 5.6e-44;
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
Db 21 DIQMTQTSSLSASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 108
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 128

RESULT 8
US-08-487-761-13
; Sequence 13, Application US/08487761
; Patent No. 6217866
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Givol, David
; APPLICANT: Bellot, Francoise
; APPLICANT: Kris, Richard
; APPLICANT: Ricca, George A.
; APPLICANT: Cheadle, Christopher
; APPLICANT: South, Victoria J.
; TITLE OF INVENTION: Monoclonal Antibodies Specific to Human
; TITLE OF INVENTION: Epidermal Growth Factor Receptor and Therapeutic Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,761
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,411
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A0207C-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-761-13

Query Match 87.1%; Score 498; DB 3; Length 112;
Best Local Similarity 87.0%; Pred. No. 1.2e-43;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPSASLGRVTISCSASQDISNYLNWYQKPDGTGTVKLLIFYSSNLHSGVPS 60
DB 1 EIHMTQTSSLSASLGRVTISCSASQDIRNYLNWYQKPDGTGTVKLLIYTTSLHSGVPS 60
QY 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
DB 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108

RESULT 10
US-09-386-658A-4
Sequence 4, Application US/09386658A
Patent No. 6593137
GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard F.
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575/54182
CURRENT APPLICATION NUMBER: US/09/386,658A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Mouse
US-09-386-658A-4

Query Match 86.9%; Score 497; DB 4; Length 109;
Best Local Similarity 86.1%; Pred. No. 1.5e-43;
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPSASLGRVTISCSASQDISNYLNWYQKPDGTGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGRVTISCSASQDIRNYLNWYQKPDGTGTVKLLIYTTSLHSGVPS 60

QY 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
DB 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108

RESULT 11
US-09-232-290-21
Sequence 21, Application US/092322290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONEGGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 108
TYPE: PRT
ORGANISM: Murine
US-09-232-290-21

Query Match 85.7%; Score 490; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 7.5e-43;
Matches 96; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPSASLGRVTISCSASQDISNYLNWYQKPDGTGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGRVTISCSASQDISNYLNWYQKPDGTGTVKLLIYTTSLHSGVPS 60
QY 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
DB 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108

RESULT 12
US-08-458-516-9
Sequence 9, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-9

Query Match 85.3%; Score 488; DB 1; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.2e-42;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLSHGVPVS 60
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDINNLYNWKPDGIVKLLIYVTSLSHGVPVS 60
QY 61 RPSGGSGTDYSLTISNLEPEDYATYFCHQYKSLPWTFGGTTKLEIK 107
Db 61 RPSGGSGTDYSLTISNLEQEDYATYFCQOGNTLPWTFGGTTKLEIK 107

RESULT 13
US-08-458-516-5
Sequence 5, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-5

Query Match 85.3%; Score 488; DB 1; Length 127;
Best Local Similarity 86.9%; Pred. No. 1.5e-42;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLSHGVPVS 60
Db 21 DIQMTQTSSLSASLGDRVTISCRASQDINNLYNWKPDGIVKLLIYVTSLSHGVPVS 80
QY 61 RPSGGSGTDYSLTISNLEPEDYATYFCHQYKSLPWTFGGTTKLEIK 107
Db 81 RPSGGSGTDYSLTISNLEQEDYATYFCQOGNTLPWTFGGTTKLEIK 127

RESULT 14
US-08-649-100-17
Sequence 17, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-PAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-PAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-17

Query Match 85.3%; Score 488; DB 3; Length 127;
Best Local Similarity 87.9%; Pred. No. 1.5e-42;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLSHGVPVS 60
Db 21 DIQMTQTSSLSASLGDRVTISCRASQDINNLYNWKPDGIVKLLIYVTSLSHGVPVS 80
QY 61 RPSGGSGTDYSLTISNLEPEDYATYFCHQYKSLPWTFGGTTKLEIK 107
Db 81 RPSGGSGTDYSLTISNLEQEDYATYFCQOGNTLPWTFGGTTKLEIK 127

RESULT 15
US-09-199-149-7
Sequence 7, Application US/09199149
Patent No. 6160099
GENERAL INFORMATION:
APPLICANT: Jonak, Zdenka L.

; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen H.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 108
; TYPE: PRT
; ORGANISM: murine cells
US-09-199-149-7

Query Match 85.1%; Score 487; DB 3; Length 108;
Best Local Similarity 85.2%; Pred. No. 1.5e-42;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
Qy 1 DIQWTQTASSLPASLGRVITISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQWTQTSSLSASLGRVITICRSSQDISNFLNWYQKPDGTVKLLIYYTSTLHSGVPS 60
Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYKLPWTFGGGTKEIKR 108
Db 61 RFSGGSGTDYSLTISNLEQEDIATYFCQGGNTLPWTFGGGTNLEIKR 108

Search completed: August 1, 2005, 09:20:55
Job time : 9.19913 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 28.4953 Seconds
(without alignments)
1476.651 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIOMTOTASSLPASLGRVT.....HOYSKLPTWGGTKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	100.0	128	9	US-09-764-304-10
2	572	100.0	128	9	US-09-764-304-19
3	572	100.0	128	14	US-10-265-713-10
4	572	100.0	128	14	US-10-265-713-19
5	572	100.0	128	14	US-10-166-626-10
6	572	100.0	128	14	US-10-166-626-19
7	510	89.2	108	9	US-09-056-1608-10
8	510	89.2	108	14	US-10-234-671-10
9	510	89.2	108	17	US-10-974-591-10
10	507	88.6	214	18	US-10-683-815-6
11	504	88.1	107	18	US-10-938-992-13
					Sequence 10, Appl
					Sequence 19, Appl
					Sequence 10, Appl
					Sequence 19, Appl
					Sequence 10, Appl
					Sequence 19, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 6, Appl
					Sequence 13, Appl

12	502	87.8	131	8	US-08-779-784-21	Sequence 21, Appl
13	502	87.8	131	14	US-10-010-729-64	Sequence 64, Appl
14	497	86.9	107	18	US-10-938-992-17	Sequence 17, Appl
15	497	86.9	109	14	US-10-197-080-4	Sequence 4, Appl
16	497	86.9	109	17	US-10-484-031-4	Sequence 4, Appl
17	494	86.4	107	16	US-10-741-657A-16	Sequence 16, Appl
18	491	85.8	107	16	US-10-473-977-69	Sequence 69, Appl
19	490	85.7	107	17	US-10-490-535-4	Sequence 4, Appl
20	490	85.7	731	20	US-11-035-599-51	Sequence 51, Appl
21	488	85.3	107	15	US-10-411-037-52	Sequence 52, Appl
22	488	85.3	107	15	US-10-411-026-52	Sequence 52, Appl
23	488	85.3	107	15	US-10-410-962-52	Sequence 52, Appl
24	488	85.3	107	16	US-10-411-049-52	Sequence 52, Appl
25	488	85.3	107	16	US-10-410-930-52	Sequence 52, Appl
26	488	85.3	107	16	US-10-410-997-52	Sequence 52, Appl
27	488	85.3	107	16	US-10-411-012-52	Sequence 52, Appl
28	488	85.3	107	16	US-10-287-994-52	Sequence 52, Appl
29	488	85.3	107	16	US-10-410-913-52	Sequence 52, Appl
30	488	85.3	107	17	US-10-410-980-52	Sequence 52, Appl
31	488	85.3	107	17	US-10-410-897-52	Sequence 52, Appl
32	488	85.3	107	17	US-10-492-261-52	Sequence 52, Appl
33	488	85.3	108	13	US-10-140-555-4	Sequence 4, Appl
34	488	85.3	127	14	US-10-084-139-2	Sequence 2, Appl
35	488	85.3	601	9	US-09-480-236-1	Sequence 1, Appl
36	488	85.3	637	16	US-10-296-085A-16	Sequence 16, Appl
37	488	85.3	638	16	US-10-296-085A-21	Sequence 21, Appl
38	488	85.3	642	16	US-10-296-085A-38	Sequence 38, Appl
39	488	85.3	642	17	US-10-496-179-6	Sequence 6, Appl
40	488	85.3	643	16	US-10-296-085A-69	Sequence 69, Appl
41	488	85.3	643	17	US-10-496-179-1	Sequence 1, Appl
42	488	85.3	656	16	US-10-296-085A-39	Sequence 39, Appl
43	488	85.3	657	16	US-10-296-085A-68	Sequence 68, Appl
44	487	85.1	108	14	US-10-141-908-7	Sequence 7, Appl
45	487	85.1	274	9	US-09-813-659-30	Sequence 30, Appl
46	487	85.1	274	15	US-10-283-610A-30	Sequence 30, Appl
47	487	85.1	302	9	US-09-813-659-18	Sequence 18, Appl
48	487	85.1	302	9	US-09-813-659-32	Sequence 32, Appl
49	487	85.1	302	15	US-10-283-610A-18	Sequence 18, Appl
50	487	85.1	302	15	US-10-283-610A-32	Sequence 32, Appl
51	487	85.1	504	14	US-10-207-655-348	Sequence 348, App
52	487	85.1	504	18	US-10-627-556-113	Sequence 113, App
53	487	85.1	555	15	US-10-107-991B-3	Sequence 3, Appl
54	487	85.1	555	18	US-10-627-556-444	Sequence 444, App
55	487	85.1	555	18	US-10-627-556-512	Sequence 512, App
56	485	84.8	107	15	US-10-310-674A-34	Sequence 34, Appl
57	485	84.8	107	15	US-10-389-679-10	Sequence 10, Appl
58	484	84.6	107	14	US-10-263-010-2	Sequence 2, Appl
59	484	84.6	127	14	US-10-268-883-6	Sequence 6, Appl
60	484	84.6	127	14	US-10-268-883-5	Sequence 5, Appl
61	483	84.4	127	16	US-10-835-641-16	Sequence 16, Appl
62	483	84.4	127	18	US-10-837-904-37	Sequence 37, Appl
63	483	84.4	652	16	US-10-296-085A-120	Sequence 120, App
64	483	84.4	895	16	US-10-296-085A-19	Sequence 19, Appl
65	483	84.4	895	16	US-10-296-085A-20	Sequence 20, Appl
66	483	84.4	895	16	US-10-296-085A-27	Sequence 27, Appl
67	483	84.4	895	17	US-10-496-179-4	Sequence 4, Appl
68	483	84.4	896	16	US-10-296-085A-17	Sequence 17, Appl
69	483	84.4	896	16	US-10-296-085A-18	Sequence 18, Appl
70	483	84.4	896	16	US-10-296-085A-26	Sequence 26, Appl
71	483	84.4	896	17	US-10-496-179-2	Sequence 2, Appl
72	483	84.4	896	17	US-10-496-179-3	Sequence 3, Appl
73	483	84.4	896	17	US-10-496-179-7	Sequence 7, Appl
74	483	84.4	899	16	US-10-296-085A-28	Sequence 28, Appl
75	483	84.4	899	17	US-10-496-179-5	Sequence 5, Appl
76	482	84.3	107	14	US-10-011-931-4	Sequence 4, Appl
77	482	84.3	107	17	US-10-985-299-4	Sequence 4, Appl
78	480.5	84.0	107	15	US-10-460-598-7	Sequence 7, Appl
79	479	83.7	247	15	US-10-620-278-21	Sequence 21, Appl
80	479	83.7	247	17	US-10-620-049-21	Sequence 21, Appl
81	476	83.2	99	16	US-10-697-399-6	Sequence 6, Appl
82	476	83.2	127	18	US-10-837-904-29	Sequence 29, Appl
83	472	82.5	634	16	US-10-416-011-2	Sequence 2, Appl
84	469	82.0	214	9	US-09-754-998-1	Sequence 1, Appl

85 469 82.0 214 16 US-10-835-641-24
86 468 81.8 233 16 US-10-660-128-9
87 465 81.3 247 15 US-10-620-278-23
88 465 81.3 247 17 US-10-620-049-23
89 462 80.8 247 15 US-10-620-278-25
90 462 80.8 247 17 US-10-620-049-25
91 453 79.2 110 9 US-09-056-1608-103
92 453 79.2 110 14 US-10-234-671-101
93 453 79.2 110 17 US-10-974-591-101
94 453 79.2 237 9 US-09-056-1608-100
95 453 79.2 237 14 US-10-234-671-100
96 453 79.2 237 17 US-10-974-591-100
97 453 79.2 491 13 US-10-011-125-2
98 452 79.0 108 18 US-10-683-815-19
99 452 79.0 108 18 US-10-496-869-33
100 451 78.8 107 9 US-09-056-1608-15

ALIGNMENTS

RESULT 1

US-09-764-304-10

; Sequence 10, Application US/09764304

; Patent No. US20020026036A1

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: HASEGAWA, MAMORU

; APPLICANT: MIYAJI, HIROMASA

; APPLICANT: KUMANA, YOSHIHISA

; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY

; FILE REFERENCE: 249-101

; CURRENT APPLICATION NUMBER: US/09/764,304

; CURRENT FILING DATE: 2001-01-19

; EARLIER APPLICATION NUMBER: 09/225,322

; EARLIER FILING DATE: 1999-01-05

; EARLIER APPLICATION NUMBER: US 08/454,680

; EARLIER FILING DATE: 1995-05-31

; EARLIER APPLICATION NUMBER: US 08/408,133

; EARLIER FILING DATE: 1995-03-21

; EARLIER APPLICATION NUMBER: US 08/292,178

; EARLIER FILING DATE: 1994-08-17

; EARLIER APPLICATION NUMBER: US07/947,674

; EARLIER FILING DATE: 1992-09-17

; EARLIER APPLICATION NUMBER: JP 3-238375

; EARLIER FILING DATE: 1991-09-18

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 128

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: CDNA KM-641

US-09-764-304-10

Query Match 100.0%; Score 572; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 108
DB 81 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 128

RESULT 2

US-09-764-304-19

; Sequence 19, Application US/09764304


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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
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Qy 61 RFSGGSGTDSYLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
Db 81 RFSGGSGTDSYLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 128

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-265-713-19

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGSGTDSYLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
Db 81 RFSGGSGTDSYLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 128
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RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGSGTDSYLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
Db 81 RFSGGSGTDSYLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 128

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
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; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-166-626-19

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 80

QY 61 RFGSGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGKLEIKR 108
DB 81 RFGSGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGKLEIKR 128

RESULT 7
US-09-056-160B-10
; Sequence 10, Application US/09056160B
; Patent No US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-10

Query Match      89.2%; Score 510; DB 9; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.4e-39;
Matches 95; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 80

QY 61 RFGSGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGKLEIKR 108
DB 81 RFGSGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGKLEIKR 128

RESULT 8
US-10-234-671-10
; Sequence 10, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-234-671-10

Query Match      89.2%; Score 510; DB 14; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.4e-39;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60

QY 61 RFGSGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGKLEIKR 108
DB 61 RFGSGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGKLEIKR 108
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RESULT 9
US-10-974-591-10
; Sequence 10, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-974-591-10
Query Match 89.2%; Score 510; DB 17; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.4e-39;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGRVTVISCSASQDISNYLNWYQKPDGTVKLLIFVSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGRVTVISCSASQDISNYLNWYQKPDGTVKLLIFVSSNLHSGVPS 60
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
Db 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
RESULT 10
US-10-683-815-6
; Sequence 6, Application US/10683815
; Publication No. US20040146512A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; LEVONWITZ, Gil
; TITLE OF INVENTION: METHODS OF TREATING ALZHEIMER'S DISEASE
; USING ANTIBODIES DIRECTED AGAINST AMYLOID BETA PEPTIDE AND

; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: 514712001500
; CURRENT APPLICATION NUMBER: US/10/683,815
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,232
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/447,611
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 60/464,754
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/480,353
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-10-683-815-6
Query Match 88.6%; Score 507; DB 18; Length 214;
Best Local Similarity 88.9%; Pred. No. 5.4e-39;
Matches 96; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGRVTVISCSASQDISNYLNWYQKPDGTVKLLIFVSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGRVTVISCSASQDISNYLNWYQKPDGTVKLLIFVSSNLHSGVPS 60
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
Db 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
RESULT 11
US-10-938-992-13
; Sequence 13, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-938-992-13
Query Match 88.1%; Score 504; DB 18; Length 107;
Best Local Similarity 86.9%; Pred. No. 4.9e-39;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGRVTVISCSASQDISNYLNWYQKPDGTVKLLIFVSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGRVTVISCSASRGINNYLNWYQKPDGTVKLLIFVSSNLHSGVPS 60
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIK 107
Db 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIK 107
RESULT 12
US-08-779-784-21
; Sequence 21, Application US/08779784
; Publication No. US20020164325A1

GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1139-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-784-21

Query Match 87.8%; Score 502; DB 8; Length 131;
Best Local Similarity 88.9%; Pred. No. 9.3e-39;
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASGLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTSSLSASGLGDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDYATYFCHQYSKLPWTFGGKLEIKR 108
DB 81 RFSGGSGTDYSLTISNLEQEDYATYFCQGNLTLPWTFGGKLEIKR 128

RESULT 13
US-10-010-729-64
Sequence 64, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
Therapeutic Uses Thereof Particularly in the Central Nervous
System
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473

PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 131
TYPE: PRT
ORGANISM: Mus musculus
US-10-010-729-64

Query Match 87.8%; Score 502; DB 14; Length 131;
Best Local Similarity 88.9%; Pred. No. 9.3e-39;
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASGLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTSSLSASGLGDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDYATYFCHQYSKLPWTFGGKLEIKR 108
DB 81 RFSGGSGTDYSLTISNLEQEDYATYFCQGNLTLPWTFGGKLEIKR 128

RESULT 14
US-10-938-992-17
Sequence 17, Application US/10938992
Publication No. US20050152903A1
GENERAL INFORMATION:
APPLICANT: Newman, Walter
APPLICANT: Qin, Shixin
APPLICANT: O'Keefe, Theresa
APPLICANT: Obar, Robert
TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REFERENCE: 3258.1033-001
CURRENT APPLICATION NUMBER: US/10/938,992
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: 60/502,568
PRIOR FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
US-10-938-992-17

Query Match 86.9%; Score 497; DB 18; Length 107;
Best Local Similarity 88.8%; Pred. No. 2.2e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASGLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASGLGDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGGSGTDYSLTISNLEPEDYATYFCHQYSKLPWTFGGKLEIKR 107
DB 61 RFSGGSGTDYSLTISNLEQEDYATYFCQGNLTLPWTFGGKLEIKR 107

RESULT 15
US-10-197-080-4
Sequence 4, Application US/10197080
Publication No. US20030113940A1
GENERAL INFORMATION:

```

; APPLICANT: Erlanger, Bernard F.
; APPLICANT: Sheetz, Michael
; APPLICANT: Brus, Louis
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NANOTUBES AND RELATED METHODS AND COMPOSITIONS
; FILE REFERENCE: 0575/67096-A
; CURRENT APPLICATION NUMBER: US/10/197,080
; CURRENT FILING DATE: 2002-07-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mouse
US-10-197-080-4

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Query Match      86.9%; Score 497; DB 14; Length 109;
Best Local Similarity 86.1%; Pred. No. 2.2e-38;
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGRVTFSCASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIQMTQTSSLSASLGRVTFSCASQDINNLYLNWYQOKPDGTVKLLIYVTSLSRSGVPS 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 RFGSGSGTDYSLTISNLEPEDATYECQYSKLPWTFGGGTKLEIKR 108
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 RFGSGSGTDYSLTINNLEPEDATYECQYSRLPFTFGSGTKLEIKR 108
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Search completed: August 1, 2005, 09:28:04
Job time : 29.4953 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.11574 Seconds
(without alignments)
1699.125 Million cell updates/sec

Title: US-10-089-500-56
Perfect score: 572
Sequence: 1 DIQWTQTASSLPASLGRVT.....HQYSKLPWTGFGTKLEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520	90.9	111	2 A38740	Ig kappa chain V r
2	514	89.9	111	2 E38740	Ig kappa chain V r
3	510	89.2	111	2 C38740	Ig kappa chain V r
4	507	88.6	107	2 B49026	Ig kappa chain V r
5	502	87.8	108	2 S69900	Ig kappa chain (cl
6	502	87.8	111	2 G38740	Ig kappa chain V r
7	498	87.1	108	1 KVM573	Ig kappa chain V r
8	495	86.5	122	2 A29380	Ig kappa chain pre
9	493	86.2	108	2 S69903	Ig kappa chain (cl
10	493	86.2	115	2 JLO080	Ig kappa chain pre
11	489	85.5	108	1 KVM5AR	Ig kappa chain pre
12	488	85.3	109	2 PH0888	Ig kappa chain V r
13	488	85.3	126	2 A34904	Ig kappa chain V r
14	485.5	84.9	108	2 S38862	Ig kappa chain V r
15	485	84.8	128	2 A26406	Ig kappa chain V r
16	484.5	84.7	107	2 S69901	Ig kappa chain (cl
17	481	84.1	107	2 A48677	Ig kappa chain V r
18	481	84.1	108	2 S69902	Ig kappa chain (cl
19	480	83.9	108	2 S19970	Ig kappa chain V r
20	478	83.6	107	2 B48677	Ig kappa chain V r
21	478	83.6	107	2 B28044	Ig kappa chain V r
22	475	83.0	107	2 A28044	Ig kappa chain V r
23	475	83.0	127	2 PH1224	Ig kappa chain pre
24	474	82.9	107	2 D48677	Ig kappa chain V-J
25	474	82.9	108	2 B26405	Ig kappa chain V r
26	473	82.7	108	2 PL0282	Ig kappa chain V r
27	473	82.7	108	2 C26405	Ig kappa chain V r
28	471.5	82.4	107	2 S69906	Ig kappa chain (cl
29	468	81.8	107	2 S32188	Ig kappa chain V r

30	466	81.5	105	2 PH0087	Ig kappa chain V r
31	462	80.8	107	2 C48677	Ig light chain V-J
32	461	80.6	108	2 S11124	Ig kappa chain V r
33	447	78.1	108	2 B30551	Ig kappa chain V r
34	429	75.0	115	2 A53276	Ig kappa chain V r
35	426	74.5	108	1 KIHUOU	Ig kappa chain V-I
36	421	73.6	93	2 S38564	Ig kappa chain V r
37	419	73.3	129	2 S52789	Ig kappa chain V r
38	408	71.3	108	1 KIHURE	Ig kappa chain V-I
39	408	71.3	127	2 S40367	Ig kappa chain V-J
40	402	70.3	108	2 B49047	Ig kappa chain V r
41	402	70.3	110	2 S44118	Ig kappa chain V-J
42	400	69.9	108	1 KIHUAG	Ig kappa chain V-I
43	399	69.8	108	1 KIHURY	Ig kappa chain V-I
44	399	69.8	131	2 S40352	Ig kappa chain V-J
45	396	69.2	108	2 S19674	Ig kappa chain V r
46	395	69.1	107	2 S36264	Ig lambda chain V
47	395	69.1	139	2 S40365	Ig kappa chain - h
48	394	68.9	130	1 KVM5M4	Ig kappa chain pre
49	391	68.4	108	2 I39154	Ig kappa chain (BR
50	391	68.4	125	2 S40333	Ig kappa chain V-J
51	388	67.8	123	2 S40331	Ig kappa chain - h
52	388	67.8	135	2 S24320	Ig kappa chain pre
53	387.5	67.7	107	2 S36275	Ig lambda chain V
54	387	67.7	106	2 PL0262	Ig kappa chain V r
55	386	67.5	109	2 S31998	Ig kappa chain - h
56	385	67.3	108	1 KIHUME	Ig kappa chain V-I
57	385	67.3	108	2 S44122	Ig kappa chain V r
58	384	67.1	106	2 PL0260	Ig kappa chain V r
59	384	67.1	111	2 I38740	Ig kappa chain V r
60	384	67.1	129	2 S40317	Ig kappa chain - h
61	384	67.1	230	2 S33161	Ig kappa chain - s
62	383	67.0	108	1 KIHUKU	Ig kappa chain V-I
63	383	67.0	129	2 S40369	Ig kappa chain - h
64	383	67.0	129	2 D32513	Ig kappa chain pre
65	382	66.8	106	2 PL0259	Ig kappa chain V r
66	382	66.8	132	2 S40334	Ig kappa chain - h
67	381	66.6	107	2 S36269	Ig lambda chain V
68	381	66.6	109	2 S31981	Ig kappa chain - h
69	381	66.6	125	2 S40349	Ig kappa chain V-J
70	381	66.6	125	2 S03365	Ig kappa chain - m
71	381	66.6	130	2 S40368	Ig kappa chain - h
72	380	66.4	108	1 KIHULY	Ig kappa chain V-I
73	380	66.4	129	2 S52793	Ig kappa chain V r
74	379.5	66.3	124	2 S40336	Ig kappa chain V-J
75	379	66.3	126	2 S40335	Ig kappa chain V-J
76	378.5	66.2	104	2 S26330	Ig kappa chain V r
77	378	66.1	107	2 S36262	Ig kappa chain V r
78	378	66.1	141	2 A49134	Ig lambda chain V
79	377	65.9	107	2 PL0270	Ig kappa chain V-I
80	377	65.9	108	1 KVM5AA	Ig kappa chain V r
81	377	65.9	127	2 S04574	Ig kappa chain pre
82	375.5	65.6	106	2 FC3997	anti-tetanus toxin
83	375.5	65.6	125	2 S40315	Ig kappa chain - h
84	375	65.6	108	4 B47271	nitrophenyl phosph
85	375	65.6	111	2 B37266	Ig kappa chain V r
86	374	65.4	108	1 KIHUBI	Ig kappa chain V-I
87	374	65.4	108	1 KIHUOU	Ig kappa chain V-I
88	374	65.4	108	1 KIHUMS	Ig kappa chain V-I
89	374	65.4	108	2 S36279	Ig lambda chain V
90	374	65.4	117	2 S42263	Ig kappa chain V r
91	374	65.4	117	2 K43528	Ig kappa chain V r
92	374	65.4	129	1 KIHUMK	Ig kappa chain pre
93	374	65.4	129	2 S32806	Ig kappa chain pre
94	373.5	65.3	106	2 C33936	Ig kappa chain V r
95	373	65.2	109	2 S31979	Ig kappa chain - h
96	373	65.2	117	2 S46371	Ig kappa chain V-J
97	372	65.0	106	2 S03303	Ig kappa chain V r
98	372	65.0	117	2 S46376	Ig kappa chain V-J
99	372	65.0	125	2 S40353	Ig kappa chain V-J
100	372	65.0	125	2 S40316	Ig kappa chain - h

Ig kappa chain V region (MOPC 173) - mouse (tentative sequence)
 C/Species: Mus musculus (house mouse)
 C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C/Accession: A01926
 R/Schiff, C.; Fougereau, M.
 Eur. J. Biochem. 59, 525-537, 1975
 A/Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid sequence of the variable region of the heavy chain.
 A/Reference number: A01926; MUID:76091934; PMID:812696
 A/Accession: A01926
 A/Molecule type: protein
 A/Residues: 1-108 <SCH>
 A/Cross-references: UNIPROT:P01643
 C/Comment: This chain was isolated from a myeloma protein.
 C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer
 F/15-90/Domain: immunoglobulin homology <IMM>
 F/23-88/Disulfide bonds: #status predicted

Query Match	87.1%;	Score 498;	DB 1;	Length 108;
Best Local Similarity	85.2%;	Pred. No. 1.1e-38;		
Matches	92;	Conservative	9;	Mismatches 7; Indels 0; Gaps 0;
Qy	1	DIQWTQTASSLPASLGRDVTISCSASQDISNLYNWYQKPDGTVKLLIFYSNLSHGVPS	60	
Db	1	DIQWTQTSSLSASLGRDVTISCSASQDISNLYNWYQKPDGTVKLLIYTSLSHGVPS	60	
Qy	61	RFSGSGSGTDYSLTISNLEPEDVATYFCHQVSKLPWTFGGGTKLEIKR	108	
Db	61	RFSGSGSGTDYSLTISLZPZBIATYCYQQYSKLPRTFGGGTKLEIKR	108	

RESULT 8
 A29380
 Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
 C/Accession: A29380
 R/Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
 J. Biol. Chem. 262, 13579-13583, 1987
 A/Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable region of the heavy chain of an anti-lymphoma monoclonal antibody.
 A/Reference number: A92612; MUID:98007582; PMID:3115981
 A/Accession: A29380
 A/Molecule type: mRNA
 A/Residues: 1-122 <CHE>
 A/Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1; PID:g196896
 C/Note: The authors translated the codon TTC for residue 1 as Leu
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/30-104/Domain: immunoglobulin homology <IMM>

Query Match	86.5%;	Score 495;	DB 2;	Length 122;
Best Local Similarity	88.0%;	Pred. No. 2.4e-38;		
Matches	95;	Conservative	3;	Mismatches 10; Indels 0; Gaps 0;
Qy	1	DIQWTQTASSLPASLGRDVTISCSASQDISNLYNWYQKPDGTVKLLIFYSNLSHGVPS	60	
Db	15	DIQWTQTSSLSASLGRDVTISCSASQDISNLYNWYQKPDGTVKLLIHYTSRLSHGVPS	74	
Qy	61	RFSGSGSGTDYSLTISNLEPEDVATYFCHQVSKLPWTFGGGTKLEIKR	108	
Db	75	RFSGSGSGTDYSLTISNLEQEDVATYFCQQGNTLPWTFGGGTKLEIKR	122	

RESULT 9
 S69903
 Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C/Accession: S69903; S69904; S69905
 R/Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
 Immunology 75, 116-121, 1992

A>Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A/Reference number: S69900; MUID:92165291; PMID:1537587
A/Accession: S69903
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WYS>
A/Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030
A/Accession: S69904
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WY2>
A/Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032
A/Accession: S69905
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <WY3>
A/Cross-references: EMBL:X55046; NID:g511033; PIDN:CAA38886.1; PID:g511034
A/Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 493; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 3.1e-38;
Matches 95; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRTVITSCASQDISNYLNWYQKPDGTVKLLIYYTSLRLHSGVPS 60

Qy 61 RFSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 61 RFSGGSGGTDYSLTISNLEQEDATYFCQGNLTPVTFGGGTKLEIKR 108

RESULT 10
JL0080
Ig kappa chain precursor V region (anti-phenylloxazalone, 18C10) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C/Accession: JL0080
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive V regions
A/Reference number: JL0076; MUID:89096973; PMID:3211160
A/Accession: JL0080
A/Molecule type: mRNA
A/Residues: 1-115 <KAA>
A/Cross-references: GB:M2793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A/Note: the authors translated the codon AGG for residue 30 as Ser
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F:7-115/Product: Ig light chain #status predicted <WAT>
F:22-96/Domain: immunoglobulin homology <IMM>
F:30-40/Region: complementarity-determining 1
F:56-62/Region: complementarity-determining 2

Query Match 86.2%; Score 493; DB 2; Length 115;
Best Local Similarity 88.0%; Pred. No. 3.4e-38;
Matches 95; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 7 DIQMTQTSSLSASLGDRTVITSCASQDISNYLNWYQKPDGTVKLLIYYTSLRLHSGVPS 66

Qy 61 RFSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 67 RFSGGSGGTDYSLTISNLEQEDATYFCQGNLTPVTFGGGTKLEIKR 114

RESULT 11
KWSAR
Ig kappa chain V regions (anti-arsenate hybridoma proteins) - mouse
C/Species: Mus musculus (house mouse)

C/Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C/Accession: A01927
R:Siegelman, M.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981
A>Title: Complete amino acid sequence of light chain variable regions derived from five non-identical light chain variable regions
A/Reference number: A01927; MUID:82150934; PMID:6801658
A/Accession: A01927
A/Molecule type: protein
A/Residues: 1-108 <SIB>
A/Cross-references: UNIPROT:P01644
A/Experimental source: strain A/J
A/Note: hp 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and 93-Ala
A/Comment: The sequence shown is HP R16.7.
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light chains held together by disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger oligomers.
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 85.5%; Score 489; DB 1; Length 108;
Best Local Similarity 88.0%; Pred. No. 7.3e-38;
Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRTVITSCASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRTVITSCASQDISNYLNWYQKPDGTVKLLIYYTSLRLHSGVPS 60

Qy 61 RFSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 61 RFSGGSGGTDYSLTISNLEQEDATYFCQGNLTPVTFGGGTKLEIKR 108

RESULT 12
PH0888
Ig kappa chain V region (anti-CD3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C/Accession: PH0888
R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
A>Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocyte antigens
A/Reference number: PH0885; MUID:92113462; PMID:1346155
A/Accession: PH0888
A/Molecule type: mRNA
A/Residues: 1-109 <SHA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 488; DB 2; Length 109;
Best Local Similarity 86.1%; Pred. No. 9.1e-38;
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRTVITSCASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRTVITSCASQDISNYLNWYQKPDGTVKLLIYYTSLRLHSGVPS 60

Qy 61 RFSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 61 KFSGGSGGTDYSLTISNLEQEDATYFCQGNLTPVTFAGGTKLEIKR 108

RESULT 13
A34904
Ig kappa chain precursor V region (5-27) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C/Accession: A34904
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A>Title: Active site structure and antigen binding properties of idiotypically cross-reactive antibodies

A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: A34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-126 <BED>
A;Cross-references: UNIPROT:Q91WF8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-109/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 488; DB 2; Length 126;
Best Local Similarity 86.8%; Pred. No. 1.1e-37;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMTOTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 20 DIQMTTSSLSASLGDRVTISCRASQDINNLYNWYQOKPDGTVKLLIYVTSKLHSGVPS 79
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGKLEIK 106
DB 80 RPSGGSGTDYSLTISNLEQEDIATYFCQGNLTPWTFGGGKLEIK 125

RESULT 14

S38862
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S38862
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
A;Accession: S38862
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <FIS>
A;Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 485.5; DB 2; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.1e-37;
Matches 94; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
QY 1 DIQMTOTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DVQMTTSSLAASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYVTSRLHSGVPS 60
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGKLEIK 107
DB 61 RPSGGSGTDYSLTISNLEQEDIATYFCQGNLTPWTFGGGKLEIK 108

RESULT 15

A26406
Ig kappa chain V region (Ars-A) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A26406
R;Sanz, I.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987
A;Title: V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination genera
A;Reference number: A26406; MUID:87147197; PMID:3103124
A;Accession: A26406
A;Molecule type: DNA
A;Residues: 1-128 <SAN>
A;Cross-references: UNIPROT:Q91WF8; GB:M15519
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 485; DB 2; Length 128;
Best Local Similarity 87.0%; Pred. No. 2e-37;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTOTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTTSSLSASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYVTSRLHSGVPS 80
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGKLEIKR 108
DB 81 RPSGGSGTDYSLTISNLEQEDIATYFCQGNALPRTFGGGTLEIKR 128

Search completed: August 1, 2005, 09:18:45
Job time : 6.11574 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 28.0249 Seconds
(without alignments)
1973.408 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIQMTTASSLPASLGDRVT.....HQVSKLPWTGGTKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	87.1	108	1 KV5K MOUSE	P01643 mus musculus
2	489	85.5	108	1 KV5K MOUSE	P01644 mus musculus
3	488	85.3	108	1 KV5L MOUSE	P01645 mus musculus
4	484	84.6	108	1 KV5N MOUSE	P01647 mus musculus
5	481	84.1	108	1 KV5M MOUSE	P01646 mus musculus
6	477	83.4	108	1 KV5O MOUSE	P01648 mus musculus
7	460	80.4	107	2 Q9JL84	Q9JL84 mus musculus
8	458	80.1	108	1 KV5U MOUSE	P01496 mus musculus
9	426	74.5	108	1 KV1B HUMAN	P01594 homo sapien
10	408	71.3	108	1 KV1O HUMAN	P01607 homo sapien
11	401	70.1	108	1 KV1X HUMAN	P01602 homo sapien
12	400	69.9	108	1 KV1A HUMAN	P01593 homo sapien
13	399	69.8	108	1 KV1P HUMAN	P01608 homo sapien
14	396	69.2	108	2 Q9UL70	Q9UL70 mus musculus
15	394.5	69.0	107	2 Q96SA9	Q96SA9 homo sapien
16	394	68.9	108	2 Q9UL77	Q9UL77 mus musculus
17	394	68.9	130	1 KV5C MOUSE	P01639 mus musculus
18	394	68.9	236	2 Q6GMX9	Q6GMX9 homo sapien
19	386	67.5	236	2 Q6GMX0	Q6GMX0 homo sapien
20	385	67.3	108	1 KV1R HUMAN	P01610 homo sapien
21	385	67.3	236	2 Q6GMW1	Q6GMW1 homo sapien
22	383	67.0	108	1 KV1L HUMAN	P01604 homo sapien
23	382	66.8	236	2 Q723Y4	Q723Y4 homo sapien
24	382	66.8	244	2 Q65ZC8	Q65ZC8 homo sapien
25	380	66.4	108	1 KV1M HUMAN	P01605 homo sapien
26	379	66.3	236	2 Q6GMX8	Q6GMX8 homo sapien
27	377	65.9	108	1 KV5P MOUSE	P01649 mus musculus
28	377	65.9	240	2 Q65ZC9	Q65ZC9 homo sapien
29	375	65.6	116	2 Q96PF6	Q96PF6 homo sapien
30	375	65.6	236	2 Q6PIH7	Q6PIH7 homo sapien
31	374	65.4	108	1 KV1C_HUMAN	P01595 homo sapien

32	374	65.4	108	1 KV1N HUMAN	P01606 homo sapien
33	374	65.4	108	1 KV1S HUMAN	P01611 homo sapien
34	374	65.4	129	1 KV1W_HUMAN	P04431 homo sapien
35	371.5	64.9	107	2 Q9UL81	Q9UL81 homo sapien
36	370	64.7	108	1 KV1H_HUMAN	P01600 homo sapien
37	370	64.7	108	1 KV1K_HUMAN	P01603 homo sapien
38	370	64.7	236	2 Q7TS98	Q7TS98 mus musculus
39	369	64.5	127	2 Q925S9	Q925S9 mus musculus
40	368	64.3	108	1 KV1E_HUMAN	P01597 homo sapien
41	368	64.3	108	1 KV1Q_HUMAN	P01609 homo sapien
42	368	64.3	108	1 KV1V_HUMAN	P04430 homo sapien
43	367	64.2	108	1 KV5S_MOUSE	P01652 mus musculus
44	366.5	64.1	109	1 KV1T_HUMAN	P01612 homo sapien
45	364.5	63.7	107	1 KV1D_HUMAN	P01596 homo sapien
46	361	63.1	108	1 KV1G_HUMAN	P01599 homo sapien
47	361	63.1	134	1 KV4C_HUMAN	P06314 homo sapien
48	360	62.9	234	2 Q72473	Q72473 homo sapien
49	359	62.8	108	2 Q9UL79	Q9UL79 homo sapien
50	359	62.8	128	1 KV5E_MOUSE	P01637 mus musculus
51	358	62.6	108	1 KV5Q_MOUSE	P01650 mus musculus
52	355	62.1	236	2 Q6PIH4	Q6PIH4 homo sapien
53	352	61.5	108	1 KV5T_MOUSE	P01653 mus musculus
54	352	61.5	238	2 Q6GJ87	Q6GJ87 mus musculus
55	351	61.4	109	2 Q920B6	Q920B6 mus musculus
56	350.5	61.3	112	2 Q8K1F3	Q8K1F3 mus musculus
57	350.5	61.3	243	2 Q7TQM2	Q7TQM2 mus musculus
58	350	61.2	236	2 Q6PIT5	Q6PIT5 mus musculus
59	349	61.0	129	1 KV1X_HUMAN	P04432 homo sapien
60	348.5	60.9	110	1 KV3P_MOUSE	P01668 mus musculus
61	347.5	60.8	134	2 Q8VDD0	Q8VDD0 mus musculus
62	347	60.7	108	1 KV5R_MOUSE	P01651 mus musculus
63	347	60.7	111	1 KV3O_MOUSE	P01667 mus musculus
64	347	60.7	111	1 KV3Q_MOUSE	P01669 mus musculus
65	346	60.5	108	1 KV1F_HUMAN	P01598 homo sapien
66	345.5	60.4	133	1 KV4B_HUMAN	P06313 homo sapien
67	345	60.3	111	1 KV3A_MOUSE	P01654 mus musculus
68	345	60.3	114	1 KV4A_HUMAN	P01625 homo sapien
69	343	60.0	108	2 Q8VIJ0	Q8VIJ0 mus musculus
70	341	59.6	111	1 KV3C_MOUSE	P01656 mus musculus
71	341	59.6	111	1 KV3L_MOUSE	P01664 mus musculus
72	341	59.6	111	2 Q920E9	Q920E9 mus musculus
73	339.5	59.4	114	2 Q8K1F1	Q8K1F1 mus musculus
74	337	58.9	111	1 KV3M_MOUSE	P01665 mus musculus
75	336	58.7	111	1 KV3D_MOUSE	P03977 mus musculus
76	336	58.7	111	1 KV3R_MOUSE	P01670 mus musculus
77	336	58.7	131	1 KV3I_MOUSE	P01661 mus musculus
78	335	58.6	111	1 KV3H_MOUSE	P01660 mus musculus
79	335	58.6	112	1 KV1I_HUMAN	P01613 homo sapien
80	335	58.6	117	1 KV1I_HUMAN	P01601 homo sapien
81	335	58.6	298	2 Q9QYF0	Q9QYF0 synthetic c
82	334	58.4	112	1 KV3G_MOUSE	P01659 mus musculus
83	333	58.2	101	2 Q9JL78	Q9JL78 mus musculus
84	333	58.2	111	1 KV3E_MOUSE	P01657 mus musculus
85	332	58.0	111	1 KV3N_MOUSE	P01666 mus musculus
86	332	58.0	132	1 KV3F_MOUSE	P01658 mus musculus
87	331.5	58.0	109	2 Q9UL78	Q9UL78 homo sapien
88	331.5	58.0	112	2 Q8K1F2	Q8K1F2 mus musculus
89	331.5	58.0	129	1 KV3M_HUMAN	P18136 homo sapien
90	331	57.9	111	1 KV3T_MOUSE	P01672 mus musculus
91	331	57.9	111	2 Q811U6	Q811U6 mus musculus
92	330.5	57.8	111	2 Q65ZN3	Q65ZN3 mus musculus
93	330	57.7	149	1 KV5A_MOUSE	P01633 mus musculus
94	329.5	57.6	113	1 KV2G_MOUSE	P01631 mus musculus
95	329	57.5	111	1 KV3S_MOUSE	P01671 mus musculus
96	327.5	57.3	241	2 Q921A6	Q921A6 mus musculus
97	327	57.2	103	2 Q9JL80	Q9JL80 mus musculus
98	327	57.2	111	1 KV3J_MOUSE	P01662 mus musculus
99	327	57.2	117	1 KV1J_HUMAN	P01602 homo sapien
100	325.5	56.9	112	1 KV3B_MOUSE	P01655 mus musculus

ALIGNMENTS

```
RESULT 1
KV5J_MOUSE
ID KV5J_MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=76091934; PubMed=812696;
RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IGC2a
immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -|- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR PIR; A01926; KVM573.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 87.1%; Score 498; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 5.4e-43;
Matches 92; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASIGDRVTISCSASQDISNYLWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTISCSASQSIGNYLBWYQKPDGTVKLLIYTSLSHSGVPS 60
QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYSKLPWTFGGKLEIKR 108
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYSKLPWTFGGKLEIKR 108

RESULT 2
KV5K_MOUSE
ID KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFP58E CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; A01927; KVM5AR.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFP597 CRC64;

Query Match 85.5%; Score 489; DB 1; Length 108;
Best Local Similarity 88.0%; Pred. No. 4.4e-42;
Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASIGDRVTISCSASQDISNYLWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTISCSASQDISNYLWYQKPDGTVKLLIYTSLSHSGVPS 60
QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYSKLPWTFGGKLEIKR 108
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYSKLPWTFGGKLEIKR 108

RESULT 3
KV5L_MOUSE
ID KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFP58E CRC64;
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Query Match      85.3%; Score 488; DB 1; Length 108;
Best Local Similarity 88.0%; Pred. No. 5.6e-42;
Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTOTASSLPASLGRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNNLHSGVPS 60
DB 1 DIQMTOTSSLSASLGRVTISCRASQDISNYLNWYQKPDGTVKLLIYYSRLHSGVPS 60

QY 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEQEDATYFCQGNMLPRTFGGTTKLEIKR 108

RESULT 4
KV5N MOUSE
ID KV5N MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEEA2 CRC64;

Query Match      84.6%; Score 484; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.4e-41;
Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTOTASSLPASLGRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNNLHSGVPS 60
DB 1 DIQMTOTSSLSASLGRVTISCRASQDISNYLNWYQKPDGTVKLLIYYSRLHSGVPS 60

QY 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEQEDATYFCQGNMLPRTFGGTTKLEIKR 108

RESULT 5
KV5M MOUSE
ID KV5M MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match      84.1%; Score 481; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 2.9e-41;
Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTOTASSLPASLGRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNNLHSGVPS 60
DB 1 DIQMTOTSSLSASLGRVTISCRASQDISNYLNWYQKPDGTVKLLIYYSRLHSGVPS 60

QY 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEQEDATYFCQGNMLPRTFGGTTKLEIKR 108

RESULT 6
KV5O MOUSE
ID KV5O MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
```

```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 Framework-1.
FT DOMAIN 35 49 Complementarity-determining-1.
FT DOMAIN 50 56 Framework-2.
FT DOMAIN 57 88 Complementarity-determining-2.
FT DOMAIN 89 97 Framework-3.
FT DOMAIN 98 108 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 83.4%; Score 477; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 7.4e-41;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRTVITSCASQDISNNYNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
Db 61 RPSGGSGTDYSLTISNLEQEDISTYFCQGNALPRTFGGKLEIKR 108

RESULT 7
Q9JL84 PRELIMINARY; PRT; 107 AA.
AC Q9JL84;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c.
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RA "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin".
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206022; AAF69320.1; -.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;

Query Match 80.4%; Score 460; DB 2; Length 107;
Best Local Similarity 81.3%; Pred. No. 4e-39;
Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRTVITSCASQDISNNYNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107
Db 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYKFPWTFGGKLEIK 107

RESULT 8
KV5U_MOUSE STANDARD; PRT; 108 AA.
AC P04946;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Ig kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-phenyloxazolone and its early diversification.";
RL Nature 304:320-324 (1983).
CC 1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; K00745; AAA38690.1; -.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 80.1%; Score 458; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 6.4e-39;
Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRTVITSCASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
Db 61 RPSGGSGTDYSLTITNLEQEDXATYXCOQGNLTPYTFGGGKLEIKR 108

RESULT 9
KVIB_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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FT HELIX      80 82
FT STRAND     84 90
FT STRAND     97 98
FT STRAND    102 106
FT NON TER    108 108
SQ SEQUENCE   108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match      71.3%; Score 408; DB 1; Length 108;
Best Local Similarity 71.3%; Pred. No. 8,1e-34;
Matches 77; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDITVNVWFQQRPGQAPKVLIVGASILETGVP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RPSGGSGTDYFTTISLQPEDIAITYCQYQSLPVTFGQTKLQITR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
KV1Y HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1WTL; X-ray; A/B=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT CONFLICT 30 31 TN -> SD (in Ref. 2).
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
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FT STRAND     19 25
FT TURN       30 31
FT STRAND     33 38
FT TURN       40 41
FT STRAND     45 49
FT TURN       50 52
FT STRAND     53 54
FT TURN       56 57
FT TURN       60 61
FT STRAND     62 67
FT TURN       68 69
FT STRAND     70 75
FT HELIX      80 82
FT STRAND     84 90
FT STRAND     98 98
FT NON TER    108 108
SQ SEQUENCE   108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match      70.1%; Score 401; DB 1; Length 108;
Best Local Similarity 68.5%; Pred. No. 4.2e-33;
Matches 74; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCASQDISNLYNWKQKPDGTVKLLIFYSSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDITVNVWFQQRPGQAPKVLIVGASILETGVP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RPSGGSGTDYFTTISLQPEDIAITYCQYQSLPVTFGQTKLQITR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
KV1A HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR PIR; A01861; K1HUAG.
DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
```

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FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 69.8%; Score 400; DB 1; Length 108;
Best Local Similarity 70.4%; Pred. No. 5.3e-33;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGRVTTISCSQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTITTCASQDISNYLWYQOKPKAPKLLIYDASNLGTGVP 60
Qy 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGTTKLEIKR 108
Db 61 RFGSGSGTDFTTISLQPEDVATYCCQYDYLPTFTFGGTTKLEIKR 108

RESULT 13
KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steimetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL York (1969).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003923; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 69.8%; Score 399; DB 1; Length 108;
Best Local Similarity 69.4%; Pred. No. 6.7e-33;
Matches 75; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGRVTTISCSQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS 60
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```
Db 1 DIQMTQSPSSLSASVGDRTITTCASQDISNYLWYQOKPKAPKLLIYDASKLEAGVPS 60
Qy 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGTTKLEIKR 108
Db 61 RFGSGSGTDFTTISLQPEDVATYCCQYDYLPTFTFGGTTKLEIKR 108

RESULT 14
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;

Query Match 69.2%; Score 396; DB 2; Length 108;
Best Local Similarity 70.4%; Pred. No. 1.4e-32;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGRVTTISCSQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTITTCASQDISNYLWYQOKPKAPKLLIYAASTLQSGVPS 60
Qy 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGTTKLEIKR 108
Db 61 RFGSGSGTDFTTISLQPEDVATYCCQYDYLPTFTFGGTTKLEIKR 108

RESULT 15
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
```

```
RL J. Immunol. 161:2020-2031 (1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match          69.0%; Score 394.5; DB 2; Length 107;
Best Local Similarity 72.5%; Pred. No. 1.9e-32;
Matches 79; Conservative 13; Mismatches 14; Indels 3; Gaps 2;

Qy 1 DIQMTQTASSLPASLGDRVTISCSAQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||: |||: |||||: |||: |||||: |||: |||||: |||: |||||: |||: |||||
Db 1 DIQMTQSPSSLASVGDRTITCRASQSISSYLNWYQQKPKGKAPKLLIYAASSLQSGVPS 60
   |||||: |||: |||||: |||: |||||: |||: |||||: |||: |||||: |||: |||||

Qy 61 RPSGGSGGTDYSLTISNLEPEDIATYFCHQ-YSKLPWTFGGGTKLEIKR 108
   |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 61 RPSGGSGGTDFTLTISLQPEDFATYCCQSYSTL--TFGGGTKVEIKR 107
   |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
```

Search completed: August 1, 2005, 09:17:10
Job time : 28.0249 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 175.288 Seconds
(without alignments)
1284.140 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVSGGDFVKPGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3071	100.0	582	4 AAB81991	Aab81991 Ganglios
2	3076	98.5	582	4 AAB81987	Aab81987 Ganglios
3	2759.5	89.9	583	4 AAB83156	Aab83156 Ganglios
4	2744.5	89.4	579	6 AAE33444	Aae33444 KS antibo
5	2738.5	89.2	579	6 AAO30910	Aao30910 di-KS-ala
6	2731.5	88.9	581	4 AAB81972	Aab81972 Ganglios
7	2715.5	88.4	575	8 ADP42961	Adp42961 Humanise
8	2592	84.4	580	6 AAO30915	Aao30915 di-NHS76
9	2560	83.4	580	6 AAO30913	Aao30913 di-NHS76
10	2234	72.7	468	8 ADQ07413	Adq07413 Mature CB
11	2234	72.7	468	8 ADQ12196	Adq12196 CBE11 pen
12	2218.5	72.2	449	5 AAO18400	Aao18400 Mature hu
13	2218.5	72.2	697	8 ADQ07403	Adq07403 hCBE11/hB
14	2218.5	72.2	697	8 ADQ12180	Adq12180 Heavy cha
15	2218.5	72.2	701	8 ADQ07409	Adq07409 hCBE11 mo
16	2218.5	72.2	701	8 ADQ12186	Adq12186 Heavy cha
17	2216	72.2	713	8 ADN97491	Adn97491 Artificia
18	2216	72.2	713	8 ADN97489	Adn97489 Artificia
19	2209.5	71.9	475	7 ADMA47075	Adm47075 Mouse ant
20	2205	71.8	477	2 AAR47453	Aar47453 chiT84.12
21	2203.5	71.8	471	8 ADM72029	Adm72029 Chimeric
22	2202	71.7	449	8 ADR23346	Adr23346 Human CD7
23	2201.5	71.7	447	6 AAE33522	Aae33522 Human AOC
24	2200.5	71.7	444	6 AAE35327	Aae35327 Humanised
25	2200.5	71.7	444	6 AAE34876	Aae34876 BIWA4/8 a

ADL15443	Humanised
ADO00851	Humanised
Aao31101	Human A2-
Aae33523	Human AOC
Adh34587	023 heavy
Abp58273	Humanised
Abp58275	Humanised
Aae33524	Human AOC
Adm72025	Chimeric
Adh34584	008 heavy
Adf11425	2D8 anti
Adp88494	Humanised
Aay68810	A rat hea
Aao14065	Heavy cha
Abu08017	Human mon
Abu08311	Humanised
Abb0109	Heavy cha
Ades4066	Humanised
Adn61714	Humanised
Aau07745	Humanised
Abp39844	Hu266 N56
Abp39848	Hu266 N56
Aau14288	Human nov
Aar24812	Sequence
Adri0018	Human pro
Adf11421	2E11 anti
Adr23344	Human CD7
Adr23352	Human CD7
Adr23354	Human CD7
Adh34586	021 heavy
Abu58807	Mucin 1 (
Abu58807	Mucin 1 (
Adr72764	Human mon
Abu08320	Humanised
Abu08320	Humanised
Abp39793	Humanised
Abbs0113	deglycosy
Ades4075	Humanised
Adf11433	16E1 anti
Adr09218	Human pro
Aar20057	Heavy cha
Adf11417	22B3 anti
Adf11429	18B2 anti
Adf11437	9H7 anti-
Adh34585	0011 heav
Aar42066	Human ant
Adma41561	Anti-inte
Aap60351	Chimeric
Aap70547	Sequence
Aay29458	Recombina
Aay29458	Recombina
Aay77766	Humanised
Abu30322	Humanised
Abu30322	Humanised
Abu59512	Humanised
Aae39094	Protein #
Adm41555	Anti-inte
Adp79584	2H7.v16 H
Adr10009	Human pro
Adr19327	Chimeric
Adr19328	Chimeric
Aaw69316	Anti-IL-8
Adr66914	Human pro
Adr66016	Human pro
Abg78151	Human Fv
Abg91842	Human ant
Adq66840	Novel hum
Adf11670	anti-CD11

99 2135 69.5 461 2 AAR42162 Anti-HIV-
100 2133.5 69.5 444 3 AAY32263 Humanised

ALIGNMENTS

RESULT 1
AAB81991
ID AAB81991 standard; protein; 582 AA.

AC AAB81991;
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
OS Synthetic.
PN WO200123432-A1.
PD 05-APR-2001.
PF 29-SEP-2000; 2000WO-JP006774.
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
DR New human type complementation-determining region-transplanted antibody,
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX Claim 39; Page 175-179; 183pp; Japanese.
PS The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX Sequence 582 AA;

Query Match 100.0%; Score 3071; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.6e-149;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYTLVESGDFVKPGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWYAYISGSGGTYY 60
DB 1 EYTLVESGDFVKPGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWYAYISGSGGTYY 60
QY 61 SDSVKGRFTISRDNANTLYLQWRSLSRSDSAMFYCTRVKLGTYVFDSWGQGTTLTVSSA 120
DB 61 SDSVKGRFTISRDNANTLYLQWRSLSRSDSAMFYCTRVKLGTYVFDSWGQGTTLTVSSA 120
QY 121 STKGVSFFPLAPSXSSTGTAALGCLVKDYFPEPVTYVSNWNSGALTSVGHPTPPAVLQSSG 180
DB 121 STKGVSFFPLAPSXSSTGTAALGCLVKDYFPEPVTYVSNWNSGALTSVGHPTPPAVLQSSG 180
QY 181 LYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKKVEPKSCDKTHTCPCPAPELLGGP 240
DB 181 LYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKKVEPKSCDKTHTCPCPAPELLGGP 240
QY 241 SVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

DB 241 SVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300
QY 301 TYRVVSULTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSRDEL 360
DB 301 TYRVVSULTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSRDEL 360
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPRPVLDSDGSGFFLYSKLTVDKSRWQ 420
DB 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPRPVLDSDGSGFFLYSKLTVDKSRWQ 420
QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLDQLQMILGINNY 480
DB 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLDQLQMILGINNY 480
QY 481 KNPKLTRLMTFKFYMPKATKELKHLQCLEELKPLEEVNLNLAQSNFHLRPRDLISINV 540
DB 481 KNPKLTRLMTFKFYMPKATKELKHLQCLEELKPLEEVNLNLAQSNFHLRPRDLISINV 540
QY 541 IVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 582
DB 541 IVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 582

RESULT 2
AAB81987
ID AAB81987 standard; protein; 582 AA.

AC AAB81987;
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
OS Synthetic.
PN WO200123432-A1.
PD 05-APR-2001.
PF 29-SEP-2000; 2000WO-JP006774.
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
DR New human type complementation-determining region-transplanted antibody,
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX Claim 41; Page 168-172; 183pp; Japanese.
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX Sequence 582 AA;

Query Match 98.5%; Score 3026; DB 4; Length 582;
Best Local Similarity 98.3%; Pred. No. 9.1e-147;
Matches 572; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVTLVESGDFVKPGSLKVSACASGAFSHYAMSWVROTAPAKLEWVAYISSGGSTYY 60
 Db 1 EVQLVESGDFVOPGGSLRVSCASGAFSHYAMSWVROAPGKLEWVAYISSGGSTYY 60
 QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGGTLLTVSSA 120
 Db 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGGTLLTVSSA 120
 QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
 Db 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
 QY 181 LYSLSVSVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELLGGP 240
 Db 181 LYSLSVSVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELLGGP 240
 QY 241 SVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300
 Db 241 SVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300
 QY 301 TYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPGRDEL 360
 Db 301 TYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPGRDEL 360
 QY 361 TKQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQ 420
 Db 361 TKQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQ 420
 QY 421 QGNVFSVSMHEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLLLDLQMLINGINNY 480
 Db 421 QGNVFSVSMHEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLLLDLQMLINGINNY 480
 QY 481 KNPKLTRMLTFKYPMPKATLKHLCLEELKPLEEVNLAKSKNPHLRPRDLISNINV 540
 Db 481 KNPKLTRMLTFKYPMPKATLKHLCLEELKPLEEVNLAKSKNPHLRPRDLISNINV 540
 QY 541 IVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 582
 Db 541 IVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 582

RESULT 3
 AAB83156
 ID AAB83156 standard; protein; 583 AA.
 AC AAB83156;
 XX
 XX
 DT 02-JUL-2001 (first entry)
 DE Ganglioside GM2 antibody-related protein #1.
 XX Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
 OS Unidentified.
 XX
 XX WO200123431-A1.
 XX
 XX PD 05-APR-2001.
 XX
 XX PF 29-SEP-2000; 2000WO-JP006775.
 XX
 XX PR 30-SEP-1999; 99JP-00278292.
 XX
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX PI Hanai N, Nakamura K, Niwa R;
 XX
 XX DR WPI; 2001-266142/27.
 XX
 XX PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
 XX radioisotopes or proteins for treatment and diagnosis of cancer.
 XX
 XX PS Claim 43; Page 61-65; 80pp; Japanese.

XX The present invention relates to derivatives of an antibody against
 CC ganglioside GM2. The antibody may be a monoclonal antibody or its
 CC fragments. The antibody is combined with a radioactive isotope, protein
 CC or small drug in the treatment and diagnosis of cancer
 XX Sequence 583 AA;
 QY 1 EVTLVESGDFVKPGSLKVSACASGAFSHYAMSWVROTAPAKLEWVAYISSGGSTYY 60
 Db 1 EVQLVESGDFVOPGGSLRVSCASGAFSHYAMSWVROAPGKLEWVAYISSGGSTYY 60
 QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGGTLLTV 117
 Db 61 NQKFKSKVTITVDSTSTAYMELHLSRSEDATVYYC--ATYGHYYGYMFAYWGGTLLTV 118
 QY 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 177
 Db 119 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 178
 QY 178 SSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELL 237
 Db 179 SSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELL 238
 QY 238 GGPSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297
 Db 239 GGPSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 298
 QY 298 YNSTYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 357
 Db 299 YNSTYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 358
 QY 358 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKS 417
 Db 359 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKS 418
 QY 418 RWQGNVFSVSMHEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLLLDLQMLINGI 477
 Db 419 RWQGNVFSVSMHEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLLLDLQMLINGI 478
 QY 478 NNYKNPKLTRMLTFKYPMPKATLKHLCLEELKPLEEVNLAKSKNPHLRPRDLISN 537
 Db 479 NNYKNPKLTRMLTFKYPMPKATLKHLCLEELKPLEEVNLAKSKNPHLRPRDLISN 538
 QY 538 INVIVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 582
 Db 539 INVIVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 583

RESULT 4
 AAE33444
 ID AAE33444 standard; protein; 579 AA.
 XX
 XX AC AAE33444;
 XX
 XX DT 02-APR-2003 (first entry)
 XX
 XX DE KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
 XX
 XX KW Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EPCAM;
 XX cancer; gene therapy; interleukin-2; IL2; fusion protein.
 XX
 XX OS Unidentified.
 XX
 XX PN WO200290566-A2.
 XX
 XX PD 14-NOV-2002.
 XX
 XX PF 03-MAY-2002; 2002WO-US013844.

```
XX 03-MAY-2001; 2001US-0289564P.
PR (LEXI-) LEXIGEN PHARM CORP.
PA
XX Gillies SD, Lo K, Qian X;
XX
XX WPI; 2003-111985/10.
DR N-P5DB; AAD51139.
XX
XX New recombinant anti-EpCAM antibody having an amino acid sequence
PT defining an immunoglobulin light or heavy chain framework region, useful
PT for the diagnosis, prognosis and treatment of cancer.
XX
XX Disclosure; Page 80-82; 82pp; English.
XX
XX The present invention relates to novel recombinant anti-EpCAM (human
CC epithelial cell adhesion molecule) antibodies comprising an amino acid
CC sequence defining an immunoglobulin light or heavy chain framework
CC region. Sequences of the present invention are useful for the diagnosis,
CC prognosis and treatment of cancer. They are also used in gene therapy.
CC The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
CC fusion protein. This sequence is used to illustrate the method of the
CC invention
XX
XX Sequence 579 AA;
SQ
Query Match 89.4%; Score 2744.5; DB 6; Length 579;
Best Local Similarity 88.5%; Pred. No. 2.2e-132;
Matches 516; Conservative 31; Mismatches 31; Indels 5; Gaps 2;
QY 1 EVTLVESGDFVKPGSLKVSAAAGFAFASHYAMSWVRQTTPAKRLEWVAYISSGSGGTYY 60
DB 1 QIQLVQSGAEVKKPGSTVKISKASGYFTTNGMNVKQTPGKGLKMGWINTYTGPTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMVFCTR-VKLGTYTFDSWGGTTLTVSS 119
DB 61 ADDFKGRFAFSLTSTAFQINNLRSEDATYFCVRFISKGDY----WQGTSTVTVSS 116
QY 120 ASTKGPSVFPFLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 179
DB 117 ASTKGPSVFPFLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 176
QY 180 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPCPAPPELLGG 239
DB 177 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPCPAPPELLGG 236
QY 240 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299
DB 237 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 296
QY 300 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 297 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356
QY 360 LTRNQVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
DB 357 MTKNQVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 416
QY 420 OQGNVFCSCVMEALHNHYTQKSLSLPGKAPTSSSTTKTQLQLHLLDLQMLINGINN 479
DB 417 OQGNVFCSCVMEALHNHYTQKSLSLPGKAPTSSSTTKTQLQLHLLDLQMLINGINN 476
QY 480 YKNPKLTRMLTFKPYMPKKATELKHQLCEEELKPLEEVNLNAQSKNPHLRPRDLISIN 539
DB 477 YKNPKLTRMLTFKPYMPKKATELKHQLCEEELKPLEEVNLNAQSKNPHLRPRDLISIN 536
QY 540 VIVLEKSETTFMCEYADETATIEVPLNRWITFCQSIISTLT 582
DB 537 VIVLEKSETTFMCEYADETATIEVPLNRWITFCQSIISTLT 579
```

```
AAO30910
ID AAO30910 standard; protein; 579 AA.
XX
XX AAO30910;
XX
XX 22-SEP-2003 (first entry)
XX
XX di-KS-ala-IL2 (D20T) variant protein.
XX
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
XX gene therapy; immunoglobulin; Ig; fusion protein; human.
XX
XX Homo sapiens.
XX Unidentified.
XX Chimeric.
XX
XX WO2003048334-A2.
XX
XX 12-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US038780.
XX
XX 04-DEC-2001; 2001US-0337113P.
XX 12-APR-2002; 2002US-0371966P.
XX
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
XX Gillies SD;
XX
XX WPI; 2003-513757/48.
XX
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
XX moiety, useful for preparing a composition for treating cancer, viral
XX infections or immune disorders.
XX
XX Example 10; Page 60-63; 71pp; English.
XX
XX The invention relates to cytokine fusion proteins with increased
XX therapeutic index and methods for increasing the therapeutic index of
XX such fusion proteins. The fusion protein comprises a non-interleukin-2
XX (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
XX composition for treating cancer, viral infections or immune disorders.
XX The fusion protein is also used in gene therapy. The present sequence is
XX di-KS-ala-IL2 (D20T) variant protein comprising di-KS heavy chain fused
XX to human IL-2 (D20T) variant protein. This sequence is used to illustrate
XX the method of the invention
XX
XX Sequence 579 AA;
SQ
Query Match 89.2%; Score 2738.5; DB 6; Length 579;
Best Local Similarity 88.3%; Pred. No. 4.4e-132;
Matches 515; Conservative 30; Mismatches 33; Indels 5; Gaps 2;
QY 1 EVTLVESGDFVKPGSLKVSAAAGFAFASHYAMSWVRQTTPAKRLEWVAYISSGSGGTYY 60
DB 1 QIQLVQSGPELKKPGSSVKISKASGYFTTNGMNVKQAPGKGLKMGWINTYTGPTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMVFCTR-VKLGTYTFDSWGGTTLTVSS 119
DB 61 ADDFKGRFTTAEETSTSTLYLQNLNRSEDATYFCVRFISKGDY----WQGTSTVTVSS 116
QY 120 ASTKGPSVFPFLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 179
DB 117 ASTKGPSVFPFLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 176
QY 180 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPCPAPPELLGG 239
DB 177 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPCPAPPELLGG 236
QY 240 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299
DB 237 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 296
```


QY 300 STYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
DB 297 STYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 356
QY 360 LTKNOVSLTCLVKGFPSPDIWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 419
DB 357 MTKNQVSLTCLVKGFPSPDIWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 416
QY 420 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDQLQMLNGINN 479
DB 417 QGNVFCSCVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLDQLQMLNGINN 476
QY 480 YKNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVNLQAQKNFHLRPRDLISIN 539
DB 477 YKNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVNLQAQKNFHLRPRDLISIN 536
QY 540 VIVLELKGSETTFMCEYADETATVIFLNRWITFCQSIISTLT 582
DB 537 VIVLELKGSETTFMCEYADETATVIFLNRWITFCQSIISTLT 579
RESULT 6
ID AAB81972 standard; protein; 581 AA.
XX AAB81972;
AC AC
DT 03-JUL-2001 (first entry)
XX Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
DE Ganglioside; GD2; complementation determining region; CDR; antibody;
XX Ganglioside; GD2; complementation determining region; CDR; antibody;
KW mouse; cancer.
XX Synthetic.
OS
PN WO200123573-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000NO-JP006773.
XX
PR 30-SEP-1999; 99JP-00278290.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266163/27.
XX
XX Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT e.g. tumors, has low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 3; Page 111-114; 123pp; Japanese.
XX
CC The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumors,
CC particularly cancer diagnosis. The present sequence is a protein used in
CC the exemplification of the invention
XX
SQ Sequence 581 AA;
Query Match 88.9%; Score 2731.5; DB 4; Length 581;
Best Local Similarity 89.0%; Pred. No. 1e-131;
Matches 518; Conservative 24; Mismatches 39; Indels 1; Gaps 1;
QY 1 EYTLVESGGDFVKPGGSLKVKCAAGFAFASHYMSWVROTPAKRLBWVAYISGGSGTY 60
DB 1 QVQLQESGPGLVKPSQTLSTITCTVSGFSLASYNIIHWVRPPGKGLWLGVIWAGGS-TNY 59

QY 61 SDSVKGRTISRDNAKNTLYLQWRSLSRSDSAMFYCTRVKLGTYTYFDSSWGQGTTLTVSSA 120
DB 60 NSALMSRLTISKDNSKNQVFLKMSLTAADTAVYYCAKESDDYDFWYMGQGLTVTVSSA 119
QY 121 STKGSPVFLAPSSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180
DB 120 STKGSPVFLAPSSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 179
QY 181 LYSLSGSVTVPPSSSLGTQYIICNVNHPKSNKTKVDKVEPKSCDKHTCCPPCPAPELLGGP 240
DB 180 LYSLSGSVTVPPSSSLGTQYIICNVNHPKSNKTKVDKVEPKSCDKHTCCPPCPAPELLGGP 239
QY 241 SVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQYNS 300
DB 240 SVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQYNS 299
QY 301 TYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
DB 300 TYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 359
QY 361 TKNQVSLTCLVKGFPSPDIWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420
DB 360 TKNQVSLTCLVKGFPSPDIWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 419
QY 421 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDQLQMLNGINN 480
DB 420 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDQLQMLNGINN 479
QY 481 KNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVNLQAQKNFHLRPRDLISIN 540
DB 480 KNPKLTRMLTFKPYMPKKATELKHLCLEBEELKPLEEVNLQAQKNFHLRPRDLISIN 539
QY 541 IVLELKGSETTFMCEYADETATVIFLNRWITFCQSIISTLT 582
DB 540 IVLELKGSETTFMCEYADETATVIFLNRWITFCQSIISTLT 581
RESULT 7
ID ADP42961 standard; protein; 575 AA.
XX ADP42961;
AC ADP42961;
DT 23-SEP-2004 (first entry)
XX
DE Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
KW immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
KW cancer; cell surface glycoephipingolipid; IL-2.
OS Synthetic.
XX
PN WO2004055056-A1.
XX
PD 01-JUL-2004.
XX
PF 16-DEC-2003; 2003WO-EP014295.
XX
PR 17-DEC-2002; 2002US-0433945P.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Gillies SD, Lo K;
XX
DR WPI; 2004-488049/46.
DR N-PSDB; ADP42959.
XX
PT New modified m14.18 antibodies with reduced immunogenicity and that
PT specifically bind the human cell surface glycoephipingolipid GD2, useful
XX for treating cancer.
PS Disclosure; SEQ ID NO 6; 51pp; English.

XX The invention relates to a novel antibody variable region, where the
CC antibody variable region specifically binds to human cell surface
CC glycosphingolipid Gb2. An antibody variable region of the invention has
CC cytostatic activity, and may have a use in gene therapy. The antibody may
CC be used for treating cancer. The nucleic acid or cell is useful for
CC manufacturing a medicament that may be used for treating diseases such as
CC cancer. The present sequence represents an immunoglobulin heavy chain-IL-
CC 2 fusion protein.
XX
XX Sequence 575 AA;

Query Match 88.4%; Score 2715.5; DB 8; Length 575;
Best Local Similarity 88.8%; Pred. No. 6.6e-131;
Matches 517; Conservative 24; Mismatches 34; Indels 7; Gaps 3;

QY 1 EVTLVESGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTAPAKRLEWVAYISSGSGTY 60
DB 1 EVQLVQSGAEVEKPGASVKISCKASGSGFTGYNMWVRQNIKSLIEWAIDPYVGGTSY 60
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSSA 120
DB 61 NQKFKGRATLVTDKSTAYMHLKSLRSEDYAVYCVS---GMEY---WGQGTSTVTVSSA 114
QY 121 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYPEPEPTVSWNSGALTSGVHTFPAVLQSSG 180
DB 115 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYPEPEPTVSWNSGALTSGVHTFPAVLQSSG 174
QY 181 LYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSKCDKTHTCPPCAPPELLGGP 240
DB 175 LYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSKCDKTHTCPPCAPPELLGGP 234
QY 241 SVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQNS 300
DB 235 SVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQNS 294
QY 301 TYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
DB 295 TYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEM 354
QY 361 TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGDFYLYSKLTVDKSRWQ 420
DB 355 TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGDFYLYSKLTVDKSRWQ 414
QY 421 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLLDQLMILNGINNY 480
DB 415 QGNVFCSCVMHEALHNHYTQKSLSLSPG--APTSSSTTKTQLQLEHLLDQLMILNGINNY 473
QY 481 KNPKLTRMLTFKPYMPKKATELKHQCLEELKPLEEVLNLAQSKNFHLRPRDLISNIN 540
DB 474 KNPKLTRMLTFKPYMPKKATELKHQCLEELKPLEEVLNLAQSKNFHLRPRDLISNIN 533
QY 541 IVLELKGSETTFCWCEYADETATVIFFLNRWITFCQSIISTLT 582
DB 534 IVLELKGSETTFCWCEYADETATVIFFLNRWITFCQSIISTLT 575

RESULT 8
AAO30915
ID AAO30915 standard; protein; 580 AA.
XX AAO30915;
XX
XX 22-SEP-2003 (first entry)
DE di-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein.
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
XX
XX Homo sapiens.
OS Unidentified.
OS Chimeric.

XX PN WO2003048334-A2.
XX PD 12-JUN-2003.
XX PF 04-DEC-2002; 2002WO-US038780.
XX PR 04-DEC-2001; 2001US-0337113P.
XX PR 12-APR-2002; 2002US-0371966P.
XX PA (EMDL-) EMD LEXIGEN RES CENT CORP.
XX PI Gillies SD;
XX WPI; 2003-513757/48.
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT moiety, useful for preparing a composition for treating cancer, viral
PT infections or immune disorders.
XX
PS Example 10; Page 68-71; 71pp; English.
CC The invention relates to cytokine fusion proteins with increased
CC therapeutic index and methods for increasing the therapeutic index of
CC such fusion proteins. The fusion protein comprises a non-interleukin-2
CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC composition for treating cancer, viral infections or immune disorders.
CC The fusion protein is also used in gene therapy. The present sequence is
CC di-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising di-
CC KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
CC is used to illustrate the method of the invention
XX
XX Sequence 580 AA;

Query Match 84.4%; Score 2592; DB 6; Length 580;
Best Local Similarity 84.7%; Pred. No. 1.4e-124;
Matches 494; Conservative 31; Mismatches 54; Indels 4; Gaps 3;

QY 1 EVTLVESGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTAPAKRLEWVAYISSGSGTY 59
DB 1 QVQLQESGPGLVKPSSETLSLTCAVSGYSISGYYWGWIRPPGKLEWIGSIYHSGS-TY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
DB 60 YNPSELKSRVTISVDTSKNQFSLKLSVTAADTAVYICARGKWSK--FDYWGQGTTLTVSS 117
QY 120 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179
DB 118 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 177
QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSKCDKTHTCPPCAPPELLGG 239
DB 178 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSKCDKTHTCPPCAPPELLGG 237
QY 240 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 299
DB 238 PSVFLFPPPKDGLMISRTPEVTCVVVDVSEDEPQVNWYVDGVEVHNKATKPREEQAQ 297
QY 300 STYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 298 STYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSQBE 357
QY 360 LTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGDFYLYSKLTVDKSRW 419
DB 358 MTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGDFYLYSKLTVDKSRW 417
QY 420 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSTTKTQLQLEHLLDQLMILNGINN 479
DB 418 QGNVFCSCVMHEALHNHYTQKSATATFGAAPTSSSTTKTQLQLEHLLDQLMILNGINN 477
QY 480 YKNPKLTRMLTFKPYMPKKATELKHQCLEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
DB 478 YKNPKLTRMLTFKPYMPKKATELKHQCLEELKPLEEVLNLAQSKNFHLRPRDLISNIN 537

Qy	540	VIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT	582
Db	538	VIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT	580
RESULT 9			
AAO30913			
ID	AAO30913	standard; protein; 580 AA.	
XX	AAO30913;		
XX			
DT	22-SEP-2003	(first entry)	
XX			
DE	dI-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) variant protein.		
XX			
KW	Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;		
KW	gene therapy; immunoglobulin; Ig; fusion protein; human; variant.		
XX			
OS	Homo sapiens.		
OS	Unidentified.		
OS	Chimeric.		
XX			
PN	W02003048334-A2.		
XX			
PD	12-JUN-2003.		
XX			
PF	04-DEC-2002; 2002WO-US038780.		
XX			
PR	04-DEC-2001; 2001US-0337113P.		
PR	12-APR-2002; 2002US-0371966P.		
XX			
PA	(EMDL-) EMD LEXIGEN RES CENT CORP.		
XX			
PI	Gallies SD;		
XX			
DR	WPI; 2003-513757/48.		
XX			
PT	New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2		
PT	moiety, useful for preparing a composition for treating cancer, viral		
PT	infections or immune disorders.		
XX			
PS	Claim 37; Page 64-67; 71pp; English.		
XX			
CC	The invention relates to cytokine fusion proteins with increased		
CC	therapeutic index and methods for increasing the therapeutic index of		
CC	such fusion proteins. The fusion protein comprises a non-interleukin-2		
CC	(IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a		
CC	composition for treating cancer, viral infections or immune disorders.		
CC	The fusion protein is also used in gene therapy. The present sequence is		
CC	dI-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising dI-		
CC	KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence		
CC	is used to illustrate the method of the invention		
XX			
SQ	Sequence 580 AA;		
Query Match			
Best Local Similarity 83.4%; Score 2560; DB 6; Length 580;			
Matches 491; Conservative 31; Mismatches 56; Indels 6; Gaps 5;			
Qy	1	EVTLVSGGDFVFKPGSLKVCASGAFASH-YAMGWVRQTPAKRLWVAYISGGSGTY	59
Db	1	QVQLQESGPGLVKRPSETLSLTCVAVSGYSISSGYWGWIRQPPGKLEWIGSIYHSGS-TY	59
Qy	60	YSDSVKGRFTISRDNAKNTLYLQWRSLSRSDSAMYECRTVRKLTGYVFDWGGQTITVSS	119
Db	60	YNFSLKSRVTVISDTSKNQSLKSLSVTAADATVYTCARGKWSK--FDYWGQGLTVTVSS	117
Qy	120	-ASTGKPSVFPPLAPSSKTSCTGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS	178
Db	118	GASTGKPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS	177
Qy	179	SGLYSLSSVVTVPSISLGTQTYICNVNHPKNTKVDKPEKSCDKTHTCPPCPAPELLG	238

Db	178	SGLYSLSSVVTVPSISLGTQTYICNVNHPKNTKVDKPEKSCDKTHTCPPCPAPP-VA	236
Qy	239	GPSVFLFPPPKPDKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY	298
Db	237	GPSVFLFPPPKPDKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQA	296
Qy	299	NSTYRVSVLTVQLQDMLNGKEYCKCKVSNKALPAPIEKTIISKAKGQPRPEQVYTLPPSRD	358
Db	297	QSTFRVSVLTVQLQDMLNGKEYCKCKVSNKGLPAPIEKTIISKAKGQPRPEQVYTLPPSRE	356
Qy	359	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR	418
Db	357	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR	416
Qy	419	WQGNVFNSSVMHEALHNHYTQKSLSLSPGKAPTSSSTTKTQLQLEHLLLDLQWLINGIN	478
Db	417	WQGNVFNSSVMHEALHNHYTQKSATATPGAAFTSSSTTKTQLQLEHLLLDLQWLINGIN	476
Qy	479	NYKNPKLTRMLTFKFMPPKATKELKHLQCLEELKPLEEVNLNLAQSKNPHLRPRDLISNI	538
Db	477	NYKNPKLTRMLTFKFMPPKATKELKHLQCLEELKPLEEVNLNLAQSKNPHLRPRDLISNI	536
Qy	539	NVIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT	582
Db	537	NVIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT	580
RESULT 10			
ADQ07413			
ID	ADQ07413	standard; protein; 468 AA.	
XX	ADQ07413;		
XX			
DT	07-OCT-2004	(first entry)	
XX			
DE	Mature CBEL1 pentameric heavy chain antibody construct.		
XX			
KW	tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;		
KW	chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;		
KW	cancer; mature heavy chain; CBEL1 pentameric.		
XX			
OS	Unidentified.		
XX			
PN	W02004058183-A2.		
XX			
PD	15-JUL-2004.		
XX			
PF	22-DEC-2003; 2003WO-US041243.		
XX			
PR	20-DEC-2002; 2002US-0435185P.		
XX			
PA	(BIOG-) BIOGEN IDEC MA INC.		
XX			
PI	Lepage D, Gill A;		
XX			
DR	WPI; 2004-525785/50.		
DR	N-PSDB; ADQ07412.		
XX			
PT	Inhibiting tumor volume comprising administering an amount of a		
PT	lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic		
PT	agent (e.g. gemcitabine or adriamycin).		
XX			
PS	Disclosure; SEQ ID NO 12; 161pp; English.		
XX			
CC	The invention relates to a novel method for inhibiting tumour volume. The		
CC	method comprises administering an amount of a lymphotoxin-beta receptor		
CC	(LT-beta-R) agonist or antibody and an amount of at least one		
CC	chemotherapeutic agent, where the administration of the LT-beta-R agonist		
CC	or antibody and the chemotherapeutic agent results in supra-additive		
CC	inhibition of the tumour. The invention further relates to: a		
CC	pharmaceutical composition comprising an amount of an LT-beta-R agonist		
CC	and at least one chemotherapeutic agent, and a pharmaceutical carrier,		

CC which upon administration to a subject results in supra-additive
CC inhibition of a tumour. The lymphotoxin-beta receptor agents have
CC cytostatic activity. Gene therapy may be used in the tumour inhibition
CC method. The method is useful for inhibiting tumour volume or for treating
CC cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic
CC agent are useful for preparing a medicament for the treatment of cancer,
CC which upon administration to a subject results in supra-additive
CC inhibition of a tumour. This sequence represents the mature CBE11
CC pentameric heavy chain antibody construct for use in the tumour volume
CC inhibition method of the invention.

XX SQ Sequence 468 AA;

Query Match 72.7%; Score 2234; DB 8; Length 468;
Best Local Similarity 93.6%; Pred. No. 2.2e-106;
Matches 424; Conservative 6; Mismatches 21; Indels 2; Gaps 2;

QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVROTAPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGGGLVKPGGSLKLSAASGFTFSDYMYWFRQTPEKRLWVATISDGGSYTY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLT-YYFDSWGQGTTLTVSS 119
DB 61 PDSVKGRTISRDNKNNLYLQMSLSKSDTAMYCVREENGNFYFDYWGQGTTLTVSS 120
QY 120 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
DB 121 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180
QY 180 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239
DB 181 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 240
QY 240 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 299
DB 241 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 300
QY 300 STYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPSRDE 359
DB 301 STYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPSRDE 360
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 419
DB 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 420
QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGKAPT 452
DB 421 QQGNVFCSCVMHEALHNHYTQKSLSLSTGK-PT 452

RESULT 11
ID ADQ12196 standard; protein; 468 AA.

XX ADQ12196;
XX ADQ12196;
XX 07-OCT-2004 (first entry)
XX CBE11 pentameric heavy chain antibody.
XX lymphotoxin-beta receptor; LT- δ gr-R; Cytostatic; cancer; tumour;
KW huCBE11; huBHA10.
XX Synthetic.
XX WO2004058191-A2.
XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US041393.
XX 20-DEC-2002; 2002US-0435154P.

PA (BIOG-) BIOGEN IDEC MA INC.
XX Garber E, Bailly V, Browning JL;
XX WPI; 2004-525790/50.
DR N-PSDB; ABQ12195.
XX New multivalent antibody constructs specific for the human lymphotoxin-
PT beta receptor, useful for diagnosing or treating cancer or for inhibiting
PT tumor volume.

XX PS Disclosure; SEQ ID NO 18; 85pp; English.

XX The present invention relates to a multivalent antibody comprising at
CC least one antigen recognition site specific for a lymphotoxin-beta
CC receptor (LT- δ gr; -R) epitope. The antibody is useful for preparing a
CC medicament for the treatment of cancer. The composition and method are
CC used for diagnosing or treating cancer and for inhibiting tumour volume.
CC The present sequence represents CBE11 pentameric heavy chain antibody.

XX Sequence 468 AA;

Query Match 72.7%; Score 2234; DB 8; Length 468;
Best Local Similarity 93.6%; Pred. No. 2.2e-106;
Matches 424; Conservative 6; Mismatches 21; Indels 2; Gaps 2;

QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVROTAPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGGGLVKPGGSLKLSAASGFTFSDYMYWFRQTPEKRLWVATISDGGSYTY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLT-YYFDSWGQGTTLTVSS 119
DB 61 PDSVKGRTISRDNKNNLYLQMSLSKSDTAMYCVREENGNFYFDYWGQGTTLTVSS 120
QY 120 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
DB 121 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180
QY 180 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239
DB 181 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 240
QY 240 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 299
DB 241 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 300
QY 300 STYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPSRDE 359
DB 301 STYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPSRDE 360
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 419
DB 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 420
QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGKAPT 452
DB 421 QQGNVFCSCVMHEALHNHYTQKSLSLSTGK-PT 452

RESULT 12
ID AAO18400 standard; protein; 449 AA.

XX AAO18400;
XX 11-OCT-2002 (first entry)
XX Mature humanised murine CBE11 heavy chain variable domain.
XX Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;
KW neoplasia; LT-beta-R; light chain; heavy chain; variable region.
XX Mus sp.

OS	Synthetic.	AC	ADQ07403;
XX	WO200230986-A2.	XX	07-OCT-2004 (first entry)
XX	18-APR-2002.	XX	hCBEl1/hBHA10 bispecific-1 antibody construct mature heavy chain.
XX	12-OCT-2001; 2001WO-US032140.	XX	tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;
XX	13-OCT-2000; 2000US-0240285P.	XX	chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;
PR	13-MAR-2001; 2001US-0275289P.	KW	cancer; mature heavy chain; hCBEl1/hBHA10 bispecific-1.
PR	21-JUN-2001; 2001US-0299987P.	XX	Homo sapiens.
XX	(BIOJ) BIOGEN INC.	OS	Synthetic.
XX	Garber E, Lyne P, Saldanha JW;	XX	WO2004058183-A2.
XX	WPI; 2002-583337/62.	PN	15-JUL-2004.
XX	New humanized anti-lymphotoxin-beta receptor antibody, useful for	XX	22-DEC-2003; 2003WO-US041243.
PT	treating or reducing the advancement, severity or effects of neoplasia,	XX	20-DEC-2002; 2002US-0435185P.
PT	particularly solid tumors (i.e. carcinomas) including colorectal cancer	PR	(BIOG-) BIOGEN IDEC MA INC.
PT	and breast cancer.	XX	Lepage D, Gill A;
XX	Example 5; Page 25-26; 41pp; English.	PI	WPI; 2004-525785/50.
XX	The present invention relates to humanised anti-lymphotoxin beta receptor	XX	DR N-PSDB; ADQ07402.
CC	(LT-beta-R) antibodies. These are derived from the murine LT-beta-R	DR	Inhibiting tumor volume comprising administering an amount of a
CC	binding antibody CBEl1 and can be used to treat neoplasia in humans. The	XX	lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic
CC	present sequence is a humanised murine CBEl1 heavy chain variable region	PT	agent (e.g. gemcitabine or adriamycin).
XX	Sequence 449 AA;	PT	Disclosure; SEQ ID NO 2; 161pp; English.
XX	Query Match 72.2%; Score 2218.5; DB 5; Length 449;	PS	The invention relates to a novel method for inhibiting tumour volume. The
XX	Best Local Similarity 93.1%; Pred. No. 1.3e-105;	XX	method comprises administering an amount of a lymphotoxin-beta receptor
XX	Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;	CC	(LT-beta-R) agonist or antibody and an amount of at least one
Qy	1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60	CC	chemotherapeutic agent, where the administration of the LT-beta-R agonist
Db	1 EVQLVESGGGLVKPGGSLRLS CAASGFTFSDYMYMFRQAPGKLEWVATISDGSVYY 60	CC	or antibody and the chemotherapeutic agent results in supra-additive
Qy	61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYFDSWGQGTTLTVSS 119	CC	inhibition of the tumour. The invention further relates to: a
Db	61 PDSVKGRFTISRDNKNSLYLQWSSLSRAEDTAVYVCAREENGNYFYFDYWGQGTTLTVSS 120	CC	pharmaceutical composition comprising an amount of an LT-beta-R agonist
Qy	120 ASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179	CC	and at least one chemotherapeutic agent, and a pharmaceutical carrier,
Db	121 ASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180	CC	which upon administration to a subject results in supra-additive
Qy	180 GLYSLSSVWTVVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELLGG 239	CC	inhibition of a tumour. The lymphotoxin-beta receptor agents have
Db	181 GLYSLSSVWTVVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELLGG 240	CC	cytostatic activity. Gene therapy may be used in the tumour inhibition
Qy	240 PSVFLPPPKDITLMSRTPEVTCVVDVSHDEPVEKFNWYDGVVEVHNAKTPREEQYN 299	CC	method. The method is useful for inhibiting tumour volume or for treating
Db	241 PSVFLPPPKDITLMSRTPEVTCVVDVSHDEPVEKFNWYDGVVEVHNAKTPREEQYN 300	CC	cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic
Qy	300 STYRVVSVLTVLHQDWLNGEKYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRDE 359	CC	agent are useful for preparing a medicament for the treatment of cancer,
Db	301 STYRVVSVLTVLHQDWLNGEKYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRDE 360	CC	which upon administration to a subject results in supra-additive
Qy	360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGFFLYSKLTVDKSRW 419	CC	inhibition of a tumour. This sequence represents the mature heavy chain
Db	361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGFFLYSKLTVDKSRW 420	CC	of the hCBEl1/hBHA10 bispecific-1 antibody construct for use in the
Qy	420 QQGNVFSCSWHEALHNNHYTKSLSPG 448	CC	tumour volume inhibition method of the invention.
Db	421 QQGNVFSCSWHEALHNNHYTKSLSPG 449	XX	Sequence 697 AA;
RESULT 13			
ADQ07403			
ID	ADQ07403 standard; protein; 697 AA.		
XX			

Db 181 GLYSLSSVVTVSSSLGTQTYICNVNHPKSNKTKVDKVKPEKSCDKTHTCCPCPAPELLGG 240
QY 240 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
Db 241 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300
QY 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRSPQVYTLPPSRDE 359
Db 301 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRSPQVYTLPPSRDE 360
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
Db 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 420
QY 420 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 448
Db 421 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 449

RESULT 14
ADQ12180
ID ADQ12180 standard; protein; 697 AA.
XX AC ADQ12180;
XX DT 07-OCT-2004 (first entry)
XX DE Heavy chain of huCBEl1/huBHA10 Bispecific-1 antibody.
XX KW lymphotoxin-beta receptor; LT- α bgf-R; Cytostatic; cancer; tumour;
XX KW huCBEl1, huBHA10.
XX OS Homo sapiens.
XX PN WO2004058191-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US041393.
XX PR 20-DEC-2002; 2002US-0435154P.
XX PA (BIOG-) BIOGEN IDEC MA INC.
XX PI Garber E, Bailly V, Browning JL;
XX DR WPI; 2004-525790/50.
XX DR N-PSDB; ADQ12179.
XX PT New multivalent antibody constructs specific for the human lymphotoxin-
PT beta receptor, useful for diagnosing or treating cancer or for inhibiting
PT tumor volume.
XX PS Claim 27; SEQ ID NO 2; 85pp; English.
XX CC The present invention relates to a multivalent antibody comprising at
CC least one antigen recognition site specific for a lymphotoxin-beta
CC receptor (LT- α bgf;-R) epitope. The antibody is useful for preparing a
CC medicament for the treatment of cancer. The composition and method are
CC used for diagnosing or treating cancer and for inhibiting tumour volume.
CC The present sequence represents mature heavy chain of huCBEl1/huBHA10
CC Bispecific-1 antibody.
XX SQ Sequence 697 AA;

Query Match 72.2%; Score 2218.5; DB 8; Length 697;
Best Local Similarity 93.1%; Pred. No. 2e-105;
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 1 EYTLVESGGDFVKGPGSLKVKSCAASGFAFASHYAMSVNRQTTPAKRLIEWAYISSGSGTYY 60
Db 1 EVQLVESGGGLVKPGGSLRLSCAASGFTPSDYMYMWRQAPGKGLEWATISDGGSTYY 60

QY 61 SDSVKGRTTISRDAKNTLYLQMSLRSEDSAMYPFCTRVKLTG-YFDSWGGTTLTVSS 119
Db 61 PDSVKGRTTISRDAKNTLYLQMSLRSEDSAMYPFCTRVKLTG-YFDSWGGTTLTVSS 120
QY 120 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVLDYFPEPVTVSNWNGALTSGVHTFPAVLQSS 179
Db 121 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVLDYFPEPVTVSNWNGALTSGVHTFPAVLQSS 180
QY 180 GLYSLSSVVTVSSSLGTQTYICNVNHPKSNKTKVDKVKPEKSCDKTHTCCPCPAPELLGG 239
Db 181 GLYSLSSVVTVSSSLGTQTYICNVNHPKSNKTKVDKVKPEKSCDKTHTCCPCPAPELLGG 240
QY 240 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
Db 241 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300
QY 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRSPQVYTLPPSRDE 359
Db 301 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRSPQVYTLPPSRDE 360
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
Db 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 420
QY 420 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 448
Db 421 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 449

RESULT 15
ADQ07409
ID ADQ07409 standard; protein; 701 AA.
XX AC ADQ07409;
XX DT 07-OCT-2004 (first entry)
XX DE hCBEl1 monospecific-1 antibody construct mature heavy chain.
XX KW tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;
XX KW chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;
XX KW cancer; mature heavy chain; hCBEl1 monospecific-1.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2004058183-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US041243.
XX PR 20-DEC-2002; 2002US-0435185P.
XX PA (BIOG-) BIOGEN IDEC MA INC.
XX PI Lepage D, Gill A;
XX WPI; 2004-525785/50.
XX DR N-PSDB; ADQ07408.
XX PT Inhibiting tumor volume comprising administering an amount of a
PT lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic
PT agent (e.g. gemcitabine or adriamycin).
XX PS Disclosure; SEQ ID NO 8; 161pp; English.
XX CC The invention relates to a novel method for inhibiting tumour volume. The
CC method comprises administering an amount of a lymphotoxin-beta receptor
CC (LT-beta-R) agonist or antibody and an amount of at least one
CC chemotherapeutic agent, where the administration of the LT-beta-R agonist
CC or antibody and the chemotherapeutic agent results in supra-additive
CC inhibition of the tumour. The invention further relates to: a

pharmaceutical composition comprising an amount of an Lr-beta-R agonist and at least one chemotherapeutic agent, and a pharmaceutical carrier, which upon administration to a subject results in supra-additive inhibition of a tumour. The lymphotoxin-beta receptor agents have cytostatic activity. Gene therapy may be used in the tumour inhibition method. The method is useful for inhibiting tumour volume or for treating cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic agent are useful for preparing a medicament for the treatment of cancer, which upon administration to a subject results in supra-additive inhibition of a tumour. This sequence represents the mature heavy chain of the hCBEL1 monospecific-1 antibody construct for use in the tumour volume inhibition method of the invention.

CC	Query Match	72.2%;	Score 2218.5;	DB 8;	Length 701;
CC	Best Local Similarity	93.1%;	Pred. No. 2e-105;		
CC	Matches 418;	Conservative	9;	Mismatches	21; Indels 1; Gaps 1;
Qy	1	EVTLVESGGDFVPGGSLKVS	CAASGPAF	SHYAMSV	ROTPAKRLEWVAYISSGGSGTYY 60
Db	1	EVQLVESGGGLVPRGGSRL	LSCAASGFT	SDYYWYF	RQAPGKGLEWVAISDGSYTY 60
Qy	61	SDSVKGRFTISRDNKNTLY	QWRSLSR	SDSAMF	CTRVKLGCT-YYPDSWGQGTTLTVSS 119
Db	61	PDSVKGRTISRDNKNSLY	QWSSLR	AEATAV	YICAREENGNYFYFDYWGQGTTLTVSS 120
Qy	120	ASTKGPSVFPLAPSSKST	SGTAAAL	GCLVKD	YFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db	121	ASTKGPSVFPLAPSSKST	SGTAAAL	GCLVKD	YFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
Qy	180	GLYSLSVSVTVPSSSLGT	QTYICNV	NHKPSNT	KVDKKVEPKSCDKTHTCPPCPAPPELLGG 239
Db	181	GLYSLSVSVTVPSSSLGT	QTYICNV	NHKPSNT	KVDKKVEPKSCDKTHTCPPCPAPPELLGG 240
Qy	240	PSVFLPPPKDITLMISRT	PEVTCV	VVDVSH	EDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
Db	241	PSVFLPPPKDITLMISRT	PEVTCV	VVDVSH	EDPEVKFNWYVDGVEVHNAKTKPREEQYN 300
Qy	300	STYRVSVLTIVLHODWL	NGKEYCK	KYSNKA	LPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
Db	301	STYRVSVLTIVLHODWL	NGKEYCK	KYSNKA	LPAPIEKTISKAKGQPREPOVYTLPPSRDE 360
Qy	360	LTKNQVSLTCLVKGFYPS	DI	AVESNG	QPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 419
Db	361	LTKNQVSLTCLVKGFYPS	DI	AVESNG	QPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 420
Qy	420	QQGNVFSCSVMHEALHN	HYTKSL	SLSPG	448
Db	421	QQGNVFSCSVMHEALHN	HYTKSL	SLSPG	449

Search completed: August 1, 2005, 09:10:17
Job time : 177.288 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	2153.5	70.1	459	1	US-08-157-101A-7	Sequence 7, Appli
2	2149.5	70.0	452	3	US-09-027-449-71	Sequence 71, Appl
3	2149.5	70.0	452	3	US-09-026-985-71	Sequence 71, Appl
4	2149.5	70.0	452	4	US-08-121-952A-71	Sequence 71, Appl
5	2149.5	70.0	452	4	US-09-234-340A-71	Sequence 71, Appl
6	2124	69.2	453	3	US-08-466-151-8	Sequence 8, Appli
7	2124	69.2	453	3	US-08-466-163B-8	Sequence 8, Appli
8	2124	69.2	453	3	US-09-802-096-8	Sequence 8, Appli
9	2124	69.2	453	4	US-09-802-077-8	Sequence 8, Appli
10	2122	69.1	451	2	US-08-887-352B-14	Sequence 14, Appl
11	2122	69.1	451	2	US-08-887-352B-16	Sequence 16, Appl
12	2122	69.1	451	3	US-08-466-151-65	Sequence 65, Appl
13	2122	69.1	451	3	US-09-109-207C-14	Sequence 14, Appl
14	2122	69.1	451	3	US-09-109-207C-16	Sequence 16, Appl
15	2122	69.1	451	3	US-09-296-005-14	Sequence 14, Appl
16	2122	69.1	451	3	US-09-296-005-16	Sequence 16, Appl
17	2122	69.1	451	4	US-09-920-171-14	Sequence 14, Appl
18	2122	69.1	451	4	US-09-920-171-16	Sequence 16, Appl
19	2122	69.1	451	4	US-09-716-028-14	Sequence 14, Appl
20	2122	69.1	451	4	US-09-716-028-16	Sequence 16, Appl
21	2122	69.1	451	4	US-10-113-996-14	Sequence 14, Appl
22	2122	69.1	451	4	US-10-113-996-16	Sequence 16, Appl
23	2118	69.0	451	2	US-08-887-352B-18	Sequence 18, Appl
24	2118	69.0	451	3	US-09-207C-18	Sequence 2, Appli
25	2118	69.0	451	3	US-09-282-505-2	Sequence 2, Appli
26	2118	69.0	451	3	US-09-054-255-2	Sequence 2, Appli
27	2118	69.0	451	3	US-09-296-005-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEFAX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-157-101A-7

Query Match 70.1%; Score 2153.5; DB 1; Length 459;
Best Local Similarity 89.8%; Pred. No. 1.4e-159;
Matches 404; Conservative 20; Mismatches 25; Indels 1; Gaps 1;
QY 1 EYTLVESGGDFVKPGSLKVSAAAGFAFHYAMSWVRQTPAKRLEWVAYISGGSGTY 60
DB 10 QQLVESGGVVPQGRSLRLSCAASGFTFSNMSHWRQAPGKGLWVAVILYDGNHKFY 69
QY 61 SDSVKGRFTISRDNKNTLYLQMRLSRSDSAMYFCTRVK-LGTYTFDSWGQGLTLTVSS 119
DB 70 ADSVKGRTISRDNKNTLYLQVSLRSLQEDTGVYICIRDTQTVGRFDSWGQGLTLTVSS 129
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 179
DB 130 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 189
QY 180 GLYSLSVVTVPSLSIGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELVGG 239
DB 190 GLYSLSVVTVPSLSIGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELVGG 249
QY 240 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 299

DB 250 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 309
QY 300 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGPPEQVYITLPPSRDE 359
DB 310 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGPPEQVYITLPPSRDE 369
QY 360 LTKNQVSLTCLVKGPYPSPDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 419
DB 370 LTKNQVSLTCLVKGPYPSPDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 429
QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 430 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 459
RESULT 2
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-71

Query Match 70.0%; Score 2149.5; DB 3; Length 452;
Best Local Similarity 88.7%; Pred. No. 2.9e-159;
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;
QY 1 EYTLVESGGDFVKPGSLKVSAAAGFAFHYAMSWVRQTPAKRLEWVAYISGGSGTY 60
DB 1 EVQLVQSGGVLVQPGGSLRLSCAASGYSFSSHYHWVRQAPGKGLWVGYIDPSNGETTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMSLSRSDSAMYFCTRVKL---GTYTFDSWGQGLTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMNSLRADTAVTYCARGDYRYNGDFVWVGQGLTVTV 120


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; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-71

Query Match      70.0%; Score 2149.5; DB 4; Length 452;
Best Local Similarity 88.7%; Pred. No. 2.9e-159;
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

QY 1 EWTLVESGGDFVKPGSLKVSAAAGFAPFASHYAMSWRQTPAKRLEWVAYISSGSGGY 60
DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFHHYHWRQAPGKGLIEWGYIDPSNGET 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMVFCRTVKL---GTYFFDSWGQGTTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMNLSRAEDTAVVYCARGDYRYNGDWFDFVWGQGTTLTV 120
QY 118 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 177
DB 121 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 180
QY 178 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKTKVKKVPEKVDGVVHNAKTKPREEQ 237
DB 181 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKTKVKKVPEKVDGVVHNAKTKPREEQ 240
QY 238 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 241 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
QY 298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 357
DB 301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417
DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 420
QY 418 RWOQGNVFSCSWMEALHNHYTKQSLSPGK 449
DB 421 RWOQGNVFSCSWMEALHNHYTKQSLSPGK 452

RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsai, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
```

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-234-340A-71

Query Match      70.0%; Score 2149.5; DB 4; Length 452;
Best Local Similarity 88.7%; Pred. No. 2.9e-159;
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

QY 1 EWTLVESGGDFVKPGSLKVSAAAGFAPFASHYAMSWRQTPAKRLEWVAYISSGSGGY 60
DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFHHYHWRQAPGKGLIEWGYIDPSNGET 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMVFCRTVKL---GTYFFDSWGQGTTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMNLSRAEDTAVVYCARGDYRYNGDWFDFVWGQGTTLTV 120
QY 118 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 177
DB 121 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 180
QY 178 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKTKVKKVPEKVDGVVHNAKTKPREEQ 237
DB 181 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKTKVKKVPEKVDGVVHNAKTKPREEQ 240
QY 238 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 241 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
QY 298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 357
DB 301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417
DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 420
QY 418 RWOQGNVFSCSWMEALHNHYTKQSLSPGK 449
DB 421 RWOQGNVFSCSWMEALHNHYTKQSLSPGK 452

RESULT 6
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
```

```

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-8

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Query Match      69.2%; Score 2124; DB 3; Length 453;
Best Local Similarity 88.8%; Pred. No. 2.8e-157;
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;

Qy 1 EYTLVSGGDFVFKPGGSLKVS CAASGFAP--SHYAMSWVRQTPAKRLWVAYISSGSGTY 59
Db 1 EVQLVESGGGLVQPGGSLRLS CAVGSYIS TSGYSWNIROAPGKLEWVASITYDGS-TN 59

Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCYTRVK--LGTYYFDSSWGQGTTLTV 117
Db 60 YADSVKGRFTISRDDSKNTFYLMNSLRADTA VYICARGSHYFGHWHFAVMQGTTLTV 119

Qy 118 SSAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
Db 120 SSASTKGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy 176 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPCPAP 235
Db 180 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPCPAP 239

Qy 236 LLGGPSVFLPAPSKPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNKTKPRE 295
Db 240 LLGGPSVFLPAPSKPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNKTKPRE 299

Qy 296 EQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 355
Db 300 EQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 359

Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVD 415
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVD 419

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Qy 416 KSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 449
Db 420 KSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 453

RESULT 7
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
; US-08-466-163B-8

```

```

Query Match      69.2%; Score 2124; DB 3; Length 453;
Best Local Similarity 88.8%; Pred. No. 2.8e-157;
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;

Qy 1 EYTLVSGGDFVFKPGGSLKVS CAASGFAP--SHYAMSWVRQTPAKRLWVAYISSGSGTY 59
Db 1 EVQLVESGGGLVQPGGSLRLS CAVGSYIS TSGYSWNIROAPGKLEWVASITYDGS-TN 59

Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCYTRVK--LGTYYFDSSWGQGTTLTV 117
Db 60 YADSVKGRFTISRDDSKNTFYLMNSLRADTA VYICARGSHYFGHWHFAVMQGTTLTV 119

Qy 118 SSAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
Db 120 SSASTKGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy 176 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPCPAP 235
Db 180 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPCPAP 239

Qy 236 LLGGPSVFLPAPSKPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNKTKPRE 295
Db 240 LLGGPSVFLPAPSKPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNKTKPRE 299

Qy 296 EQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 355
Db 300 EQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 359

Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVD 415
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVD 419

RESULT 8
US-09-802-096-8
; Sequence 8, Application US/09802096

```

; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P07182CJUS
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-096-8

Query Match 69.2%; Score 2124; DB 4; Length 453;
Best Local Similarity 88.8%; Pred. No. 2.8e-157;
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;
QY 1 EVTLVESGGDFVKPGSLKVSAAAGPAP-SHYAMSWVRQTPAKLEWVAYISSGSGTY 59
DB 1 EVQLVESGGGLVQPGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITYDGS-TN 59
QY 60 YDSVKGRFTISRDAKNTLYLQMSLRSEDSAMVFCFTRVK--LGTYVFDMSGQGTTLTV 117
DB 60 YADSVKGRFTISRDDSKNTFYLQNSLRADETAVYICARGSHYFGHWFAVWGQGTTLTV 119
QY 118 SSAST--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 175
DB 120 SSASTKGKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 179
QY 176 LQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPE 235
DB 180 LQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPE 239
QY 236 LGGPSVFLPFPKPKDNLMIKRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
DB 240 LGGPSVFLPFPKPKDNLMIKRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 299
QY 296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
DB 300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 415
DB 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 419
QY 416 KSRWQOGNVFSCVMHEALHNHYTOKSLSPGK 449
DB 420 KSRWQOGNVFSCVMHEALHNHYTOKSLSPGK 453

RESULT 9
US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. 6659472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P07182CJUS

; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

Query Match 69.2%; Score 2124; DB 4; Length 453;
Best Local Similarity 88.8%; Pred. No. 2.8e-157;
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;
QY 1 EVTLVESGGDFVKPGSLKVSAAAGPAP-SHYAMSWVRQTPAKLEWVAYISSGSGTY 59
DB 1 EVQLVESGGGLVQPGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITYDGS-TN 59
QY 60 YDSVKGRFTISRDAKNTLYLQMSLRSEDSAMVFCFTRVK--LGTYVFDMSGQGTTLTV 117
DB 60 YADSVKGRFTISRDDSKNTFYLQNSLRADETAVYICARGSHYFGHWFAVWGQGTTLTV 119
QY 118 SSAST--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 175
DB 120 SSASTKGKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 179
QY 176 LQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPE 235
DB 180 LQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPE 239
QY 236 LGGPSVFLPFPKPKDNLMIKRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
DB 240 LGGPSVFLPFPKPKDNLMIKRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 299
QY 296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
DB 300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 415
DB 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD 419
QY 416 KSRWQOGNVFSCVMHEALHNHYTOKSLSPGK 449
DB 420 KSRWQOGNVFSCVMHEALHNHYTOKSLSPGK 453

RESULT 10
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IGE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-14

Query Match 69.1%; Score 2122; DB 2; Length 451;
Best Local Similarity 88.7%; Pred. No. 4e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

QY 1 EVTLVSGGDFVKPGGSLKVSACASGAF-SHYAMSVWRTQPAKLEWVAYISSGSGTY 59
Db 1 EVQLVSGGGLVQPGGSLRSLCAVSGYSITSGYSWNIWIRQAPGKLEWVASITYDGS-TN 59
QY 60 YDSVKGRTTISRDNKNTLYLQMSLRSEDSAMYFCTRVK--LGTYFDSWGQGTTLTV 117
Db 60 YNPSVKGRTTISRDDSKNTFYLMNSLRADTAVYICARGSHYFGHHFAVWGQGTTLTV 119
QY 118 SSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 177
Db 120 SSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 179
QY 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 237
Db 180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 239
QY 238 GGPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 297
Db 240 GGPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 299
QY 298 YNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSR 357
Db 300 YNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKS 417
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKS 419
QY 418 RMOQGNVFCSCVMHEALHNNHYTKQSLSPGK 449
Db 420 RMOQGNVFCSCVMHEALHNNHYTKQSLSPGK 451

RESULT 11
US-08-887-352B-16
Sequence 16, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-16

Query Match 69.1%; Score 2122; DB 2; Length 451;
Best Local Similarity 88.7%; Pred. No. 4e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

QY 1 EVTLVSGGDFVKPGGSLKVSACASGAF-SHYAMSVWRTQPAKLEWVAYISSGSGTY 59
Db 1 EVQLVSGGGLVQPGGSLRSLCAVSGYSITSGYSWNIWIRQAPGKLEWVASITYDGS-TN 59
QY 60 YDSVKGRTTISRDNKNTLYLQMSLRSEDSAMYFCTRVK--LGTYFDSWGQGTTLTV 117
Db 60 YNPSVKGRTTISRDDSKNTFYLMNSLRADTAVYICARGSHYFGHHFAVWGQGTTLTV 119
QY 118 SSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 177
Db 120 SSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 179
QY 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 237
Db 180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 239
QY 238 GGPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 297
Db 240 GGPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 299
QY 298 YNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSR 357
Db 300 YNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKS 417
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKS 419
QY 418 RMOQGNVFCSCVMHEALHNNHYTKQSLSPGK 449
Db 420 RMOQGNVFCSCVMHEALHNNHYTKQSLSPGK 451

RESULT 12
US-08-466-151-65
Sequence 65, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
ADDRESSEE: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match 69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 4e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

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QY 1 EVTLVESGGDFVKPGGSLKVSAAAGPAP-SHYAMSWVRQTPAKLEWVAVYSSGSGCTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSWNWIRQAPGKLEWVASITYDGS-TN 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVK--LGTYVFDMSGQGTTLTV 117
DB 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHMFHAVWGQGLTVTV 119
QY 118 SSASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 177
DB 120 SSASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 179
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPCPAPPELL 237
DB 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPCPAPPELL 239
QY 238 GGPSVFLPPPKPKDMLSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 240 GGPSVFLPPPKPKDMLSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
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DB 300 YNSTYRVVSVLTVLHQLDMLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417
DB 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
QY 418 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
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RESULT 14
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:

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QY 418 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
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RESULT 13
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-14

Query Match 69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 4e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

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QY 1 EVTLVESGGDFVKPGGSLKVSAAAGPAP-SHYAMSWVRQTPAKLEWVAVYSSGSGCTY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSWNWIRQAPGKLEWVASITYDGS-TN 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVK--LGTYVFDMSGQGTTLTV 117
DB 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHMFHAVWGQGLTVTV 119
QY 118 SSASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 177
DB 120 SSASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 179
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DB 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPCPAPPELL 239
QY 238 GGPSVFLPPPKPKDMLSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
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DB 300 YNSTYRVVSVLTVLHQLDMLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSR 359
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417
DB 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419
QY 418 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
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RESULT 14
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:


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; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match      69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 4e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

Qy 1 EVTLVESGGDFVKPGGSLKVSACGAPF-SHYAMSHVROTAPAKRLWVAYISSGSGTY 59
Db 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIROAPGKLEWVASITYDGS-TN 59
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVK--LGTYYFDSWQGGTTLTV 117
Db 60 YNPSVKGRITISRDDSKNTFYLQMSLRADTAIVYCARGSHYFGHWHFAVWGQGLTVTV 119
Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQ 177
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQ 179
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Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 417
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 419
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Db 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-296-005-14
; Sequence 14. Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
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; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match      69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 4e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

Qy 1 EVTLVESGGDFVKPGGSLKVSACGAPF-SHYAMSHVROTAPAKRLWVAYISSGSGTY 59
Db 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIROAPGKLEWVASITYDGS-TN 59
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVK--LGTYYFDSWQGGTTLTV 117
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Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSR 359
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 417
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKS 419
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Job time : 45.1842 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 153.558 Seconds
(without alignments)
1476.651 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2715.5	88.4	575	16	US-10-737-208A-6
4	2592	84.4	580	14	US-10-310-719-37
5	2560	83.2	580	14	US-10-310-719-35
6	2218.5	72.2	663	15	US-10-412-406-32
7	2218.5	72.2	4852	16	US-10-412-406-33
8	2216	72.2	713	16	US-10-679-620-64
9	2216	72.2	715	16	US-10-679-620-62
10	2205	71.8	464	17	US-10-938-353-102
11	2201.5	71.7	447	15	US-10-474-832-4
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					Sequence 32, Appl
					Sequence 37, Appl
					Sequence 35, Appl
					Sequence 33, Appl
					Sequence 62, Appl
					Sequence 102, Appl
					Sequence 4, Appl

444	14	US-10-150-475A-6	Sequence 6, Appl
444	16	US-10-704-522-6	Sequence 6, Appl
444	16	US-10-645-215-6	Sequence 6, Appl
449	16	US-10-635-908-16	Sequence 18, Appl
449	16	US-10-635-908-18	Sequence 18, Appl
445	14	US-10-320-231A-79	Sequence 79, Appl
445	17	US-10-867-506-79	Sequence 79, Appl
445	17	US-10-474-832-5	Sequence 5, Appl
447	17	US-10-938-353-98	Sequence 98, Appl
470	17	US-10-476-265-12	Sequence 12, Appl
449	17	US-10-476-265-20	Sequence 20, Appl
468	17	US-10-476-265-20	Sequence 20, Appl
447	15	US-10-474-832-6	Sequence 6, Appl
446	15	US-10-408-901-38	Sequence 38, Appl
449	9	US-09-736-371B-21	Sequence 21, Appl
449	15	US-10-463-442-21	Sequence 21, Appl
474	14	US-09-848-832-3	Sequence 3, Appl
474	14	US-10-225-108A-3	Sequence 3, Appl
474	15	US-10-461-148-1	Sequence 1, Appl
453	17	US-10-891-658-41	Sequence 41, Appl
442	15	US-10-226-435A-12	Sequence 12, Appl
442	16	US-10-487-326-12	Sequence 12, Appl
442	16	US-10-486-908-12	Sequence 12, Appl
442	18	US-10-512-527-12	Sequence 12, Appl
477	15	US-10-291-265-395	Sequence 395, Appl
445	15	US-10-408-901-34	Sequence 34, Appl
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445	15	US-10-408-901-42	Sequence 42, Appl
446	15	US-10-408-901-50	Sequence 50, Appl
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452	17	US-10-861-049-16	Sequence 16, Appl
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447	16	US-10-379-392-141	Sequence 22, Appl
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451	15	US-10-423-299-4	Sequence 4, Appl
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452	17	US-10-861-049-20	Sequence 20, Appl
471	17	US-10-861-049-11	Sequence 11, Appl
472	15	US-10-108-260A-4073	Sequence 4073, Appl
447	16	US-10-379-392-143	Sequence 143, Appl
473	15	US-10-108-260A-4681	Sequence 4681, Appl
453	9	US-09-802-077-8	Sequence 8, Appl
453	9	US-09-802-096-8	Sequence 8, Appl
453	9	US-09-925-179-8	Sequence 8, Appl
453	17	US-10-968-237-8	Sequence 8, Appl
447	16	US-10-379-392-142	Sequence 142, Appl
451	9	US-09-920-171-14	Sequence 14, Appl
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451	14	US-10-113-996-16	Sequence 16, Appl

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94 2122 69.1 468 15 US-10-377-109-2 Sequence 2, Appli
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96 2122 69.1 476 17 US-10-697-995-9 Sequence 9, Appli
97 2122 69.1 667 16 US-10-764-428-7 Sequence 7, Appli
98 2122 69.1 669 16 US-10-764-428-21 Sequence 21, Appli
99 2121 69.1 472 15 US-10-108-260A-4295 Sequence 4295, Ap
100 2120.5 69.0 447 16 US-10-379-392-118 Sequence 118, App

ALIGNMENTS

RESULT 1

US-10-138-727A-41
; Sequence 41, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Susan
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/10/138,727A
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain-IL2
US-10-138-727A-41

Query Match 89.4%; Score 2744.5; DB 14; Length 579;
Best Local Similarity 88.5%; Pred. No. 1.2e-166;
Matches 516; Conservative 31; Mismatches 31; Indels 5; Gaps 2;
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWRQT PAKRL EWVAYI SSGSGSTYY 60
DB 1 QIQLVQSGAEVKKPGETVKIKSASGYFTTNYGMNVRQTPGKGLKMWGINTYTGPTY 60
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYYPDSWGQGTTLTVSS 119
DB 61 ADDFKGRFAFSLTSTAFQIINNLRSEDATATFCVRFISKGDY----WGQGTSTVTVSS 116
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179
DB 117 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176
QY 180 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239
DB 177 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 236
QY 240 PSVFLFPPKPKDRLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYN 299
DB 237 PSVFLFPPKPKDRLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYN 296
QY 300 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356

QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 419
DB 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 416
QY 420 QGQNVFSCSVNHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 479
DB 417 QGQNVFSCSVNHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 476
QY 480 YKNPKLTRLMTFKFYMPPKKATLKHLCLEBELKPLEBEVLNLAQSKNPHLRPRDLISIN 539
DB 477 YKNPKLTRLMTFKFYMPPKKATLKHLCLEBELKPLEBEVLNLAQSKNPHLRPRDLISIN 536
QY 540 VIVLELKGSETTFMCEVADEATATVEFLNRWITFCQSIISTLT 582
DB 537 VIVLELKGSETTFMCEVADEATATVEFLNRWITFCQSIISTLT 579

RESULT 2

US-10-310-719-32
; Sequence 32, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant
US-10-310-719-32

Query Match 89.2%; Score 2738.5; DB 14; Length 579;
Best Local Similarity 88.3%; Pred. No. 2.8e-166;
Matches 515; Conservative 30; Mismatches 33; Indels 5; Gaps 2;
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWRQT PAKRL EWVAYI SSGSGSTYY 60
DB 1 QIQLVQSGPELKKPGSSVKISCKASGYFTTNYGMNVRQAPGKGLKMWGINTYTGPTY 60
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYYPDSWGQGTTLTVSS 119
DB 61 ADDFKGRFTTIAETSTSTLYLQNLNRSEDATATFCVRFISKGDY----WGQGTSTVTVSS 116
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179
DB 117 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176
QY 180 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239
DB 177 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 236
QY 240 PSVFLFPPKPKDRLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYN 299
DB 237 PSVFLFPPKPKDRLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYN 296
QY 300 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 419
DB 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 416

QY 420 QGNVFCSCVMHEALHNHYTKQSLSPGKAPTSSTSKTKTQLQLEHLLDQLMILGINN 479
Db 417 QGNVFCSCVMHEALHNHYTKSATATPGAAPTSSSTKTKTQLQLEHLLDQLMILGINN 476
QY 480 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 539
Db 477 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 536
QY 540 VIVLELKGSETTFCMCEYADETATIVBFLNRWITFCOSIISTLT 582
Db 537 VIVLELKGSETTFCMCEYADETATIVBFLNRWITFCOSIISTLT 579
RESULT 3
US-10-737-208A-6
; Sequence 6, Application US/10737208A
; Publication No. US20040203100A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
; FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/433,945
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2
US-10-737-208A-6

Query Match 88.4%; Score 2715.5; DB 16; Length 575;
Best Local Similarity 88.8%; Pred. No. 8.1e-165;
Matches 517; Conservative 24; Mismatches 34; Indels 7; Gaps 3;
QY 1 EVTLVESGDFVYKPGSLKVSQASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60
Db 1 EVQLVQSGAEVKEPKGASVKISCKASGSGFTGYNMNVVRQNIQKSLWGAIDPFYGGTGY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSLRSDSAMYFCTRVKLGTYTYPDSMGQGTLLTVSSA 120
Db 61 NQKFKGRLTVDKSTSTAYMHLKLSRSDTAVIYCVS---GMEY---WGQGTSTVTVSSA 114
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
Db 115 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 174
QY 181 LYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
Db 175 LYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 234
QY 241 SVPLFPKPKDLMISRTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 300
Db 235 SVPLFPKPKDLMISRTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 294
QY 301 TYRVVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 360
Db 295 TYRVVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 354
QY 361 TKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420
Db 355 TKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 414
QY 421 QGNVFCSCVMHEALHNHYTKQSLSPGKAPTSSTSKTKTQLQLEHLLDQLMILGINN 480
Db 415 QGNVFCSCVMHEALHNHYTKQSLSPG-APTSSSTSKTKTQLQLEHLLDQLMILGINN 473
QY 481 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 540

Db 474 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 533
QY 541 VIVLELKGSETTFCMCEYADETATIVBFLNRWITFCOSIISTLT 582
Db 534 VIVLELKGSETTFCMCEYADETATIVBFLNRWITFCOSIISTLT 575
RESULT 4
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dI-NHS76(gamma4h) (FN=AQ) -ala-IL2 (D20T) heavy chain fused to
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match 84.4%; Score 2592; DB 14; Length 580;
Best Local Similarity 84.7%; Pred. No. 6.2e-157;
Matches 494; Conservative 31; Mismatches 54; Indels 4; Gaps 3;
QY 1 EVTLVESGDFVYKPGSLKVSQASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
Db 1 QVQLQESGPGLVKPKSETLSLTCAVSGYSISSGYWGWIRQPPKGLWIGSIYHSGS-TY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTRVKLGTYTYPDSMGQGTLLTVSS 119
Db 60 YNPGLSKRTISVDTSKQFSLKLSVTAADTAIVYCARQKWSK--FDYWGQGTLLTVSS 117
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
Db 118 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 177
QY 180 GLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239
Db 178 GLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 237
QY 240 PSVFLFPKPKDLMISRTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 299
Db 238 PSVFLFPKPKDLMISRTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 297
QY 300 STYRVVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 359
Db 298 STYRVVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 357
QY 360 LTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 419
Db 358 LTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 417
QY 420 QGNVFCSCVMHEALHNHYTKQSLSPGKAPTSSTSKTKTQLQLEHLLDQLMILGINN 479
Db 418 QGNVFCSCVMHEALHNHYTKSATATPGAAPTSSSTSKTKTQLQLEHLLDQLMILGINN 477
QY 480 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 539
Db 478 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 537

QY 540 VIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 582
Db 538 VIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 580

RESULT 5
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dI-NHS76(gamma2h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to IL2
; OTHER INFORMATION: variant
US-10-310-719-35

Query Match 83.4%; Score 2560; DB 14; Length 580;
Best Local Similarity 84.1%; Pred. No. 6.8e-155;
Matches 491; Conservative 31; Mismatches 56; Indels 6; Gaps 5;
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFSH-YAMSWVRQTPAKRLEWVAVYISSGGSGTY 59
Db 1 QVQLQESGFLVKPSETLSLTCANSGYISGGYWGWRQPPGKLEWIGSIYHSGS-TY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLGTYFYFDSWGGTTLTVSS 119
Db 60 YNPSLKSRTISVDTSKNQFSLKSSVTAADTAVYICARGKWSK--FDYWGQGTTLTVSS 117
QY 120 -ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 178
Db 118 GASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 177
QY 179 SGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLG 238
Db 178 SGLYSLSVVTVPSSFGTQTYTCNVDHKPSNTKVDKVEPKSCDKTHTCPPCPAPP-VA 236
QY 239 GPSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 298
Db 237 GPSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREBQA 296
QY 299 NSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 358
Db 297 QSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRE 356
QY 359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 418
Db 357 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 416
QY 419 WOQGNVFSCVMEALHNHYTQKSLSLSPGKAPTSSSTKTKQLQLEHLLDQLMTLNGIN 478
Db 417 WOQGNVFSCVMEALHNHYTQKSATATPGAAPTSSSTKTKQLQLEHLLDQLMTLNGIN 476
QY 479 NYKNPKLFRMLTFKFPYMPKKATLKHQCLEBELKPLEVLNLAQSKNPHLRPRDLISNI 538
Db 477 NYKNPKLFRMLTFKFPYMPKKATLKHQCLEBELKPLEVLNLAQSKNPHLRPRDLISNI 536
QY 539 NVIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 582
Db 537 NVIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 580

RESULT 6
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GABER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINA100CN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: RastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-412-406-32

Query Match 72.2%; Score 2218.5; DB 15; Length 663;
Best Local Similarity 93.1%; Pred. No. 4.7e-133;
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFSH-YAMSWVRQTPAKRLEWVAVYISSGGSGTY 60
Db 215 EVQLVESGGGLVKPGGSLRLSCAASGFTFSYIMYWFRQAPGKLEWATISDGSYTY 274
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLGTYFYFDSWGGTTLTVSS 119
Db 275 PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLGTYFYFDSWGGTTLTVSS 334
QY 120 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 179
Db 335 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 394
QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLG 239
Db 395 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLG 454
QY 240 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 299
Db 455 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 514
QY 300 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
Db 515 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 574
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
Db 575 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 634
QY 420 QOQGNVFSCVMEALHNHYTQKSLSLSPG 448
Db 635 QOQGNVFSCVMEALHNHYTQKSLSLSPG 663

RESULT 7
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.
APPLICANT: GARBER, Ellen
APPLICANT: LYNE, Paul
APPLICANT: SALDHANA, Jose W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINALOOCN
CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: PCT/US01/32140
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 4852
TYPE: PRT
ORGANISM: Homo Sapien
US-10-412-406-33

Query Match 72.2%; Score 2218.5; DB 15; Length 4852;
Best Local Similarity 93.1%; Pred. No. 4.8e-132;
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 1 EYTLVESGGDFVKPGGSLKVSACGFAFSPHYAMSVVROTQPAKLEWVAISSGGSTYY 60
DB 4404 EVQLVESGGDLVKPGGSLRLSCAASGFTFSYIMYFRQAPGKLEWVAISDGSSTYY 4463
QY 61 SDSVKGRTISRDNKNTLYLQMSRLSSEDSAMYFCTRVKLT-YVFDMSGQGTTLTVSS 119
DB 4464 PDSVKGRTISRDNKNTLYLQMSRLSRAEDTAVYICARENGFYFDYWGQGTTLTVSS 4523
QY 120 ASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
DB 4524 ASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 4583
QY 180 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCAPPELLGG 239
DB 4584 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCAPPELLGG 4643
QY 240 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
DB 4644 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 4703
QY 300 STYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 4704 STYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 4763
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
DB 4764 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 4823
QY 420 QQGNVFSCSVWHEALHNHYTQKSLSLSPG 448
DB 4824 QQGNVFSCSVWHEALHNHYTQKSLSLSPG 4852

RESULT 8
US-10-679-620-64
Sequence 64, Application US/10679620
Publication No. US20040110930A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Reini, Stephen J.
APPLICANT: Edwards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/10/679, 620
CURRENT FILING DATE: 2003-10-03

PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.2
SEQ ID NO 64
LENGTH: 713
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: p9E10chimericv2-1, see Example 15
US-10-679-620-64

Query Match 72.2%; Score 2216; DB 16; Length 713;
Best Local Similarity 91.7%; Pred. No. 7.4e-133;
Matches 419; Conservative 10; Mismatches 20; Indels 8; Gaps 2;

QY 1 EYTLVESGGDFVKPGGSLKVSACGFAFSPHYAMSVVROTQPAKLEWVAISSGGSTYY 60
DB 257 EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSVROTQPKRLEWVATIGSRGTYY 316
QY 61 SDSVKGRTISRDNKNTLYLQMSRLSSEDSAMYFCTRVKLT---GTYYF---DSWGQ 112
DB 317 PDSVKGRTISRDNKNTLYLQMSRLSSEDTANYICARSEFYNYGNTYYISANDYWGQ 376
QY 113 TLTVSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172
DB 377 ASVTSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 436
QY 173 PAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCP 232
DB 437 PAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCP 496
QY 233 APPELLGGSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 292
DB 497 APPELLGGSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 556
QY 293 PREEQYNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 352
DB 557 PREEQYNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 616
QY 353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 412
DB 617 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 676
QY 413 TVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPG 449
DB 677 TVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPG 713

RESULT 9
US-10-679-620-62
Sequence 62, Application US/10679620
Publication No. US20040110930A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Reini, Stephen J.
APPLICANT: Edwards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/10/679, 620
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 715
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: p9E10chimericv1-1, see Example 15
US-10-679-620-62

```
Query Match 72.2%; Score 2216; DB 16; Length 715;
Best Local Similarity 91.7%; Pred. No. 7.4e-133;
Matches 419; Conservative 10; Mismatches 20; Indels 8; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB EVDLVESGGDLVKPGGSLKLSAAAGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTYY 318
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKL-----GTYF---DSWQOQ 112
DB PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKNTYYYSAMDYWGQO 378
QY 113 TTLTVSSASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTF 172
DB ASVTVSSASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTF 438
QY 173 PAVLOSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPC 232
DB 439 PAVLOSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPC 498
QY 233 APELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 292
DB 499 APELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 558
QY 293 PREEOYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 352
DB 559 PREEOYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 618
QY 353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKL 412
DB 619 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKL 678
QY 413 TVDKSRWQOQNVFSCVMHEALHNHYTQKSLSLSPGK 449
DB 679 TVDKSRWQOQNVFSCVMHEALHNHYTQKSLSLSPGK 715

RESULT 10
US-10-938-353-102
; Sequence 102, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENSCH, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 102
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-102

Query Match 71.8%; Score 2205; DB 17; Length 464;
Best Local Similarity 92.2%; Pred. No. 2.2e-132;
Matches 414; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB 20 QVQLVESGGGLVKPGGSLRLSAAAGFTFSFYMSWIRQAPGKGLEWVSYISSGSGTY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYYFDWSWQOQTTLTVSSA 120

Query Match 71.7%; Score 2201.5; DB 15; Length 447;
Best Local Similarity 92.9%; Pred. No. 3.6e-132;
Matches 416; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGGGLVQPGGSLRLSAAAGFTFSRYTTSWVRQAPGKGLEWVATISGGGH-TYY 59
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYYFDWSWQOQTTLTVSSA 120
DB 60 LDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYYFDWSWQOQTTLTVSSA 119
QY 121 STKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSSG 180
DB 120 STKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSSG 179
QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPAPPELLGCP 240
DB 180 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPAPPELLGCP 239
QY 241 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300
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DB 80 ADSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYYFDWSWQOQTTLTVSSA 135
QY 121 STKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSSG 180
DB 136 STKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSSG 195
QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPAPPELLGCP 240
DB 196 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPAPPELLGCP 255
QY 241 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300
DB 256 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 315
QY 301 TYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPSPRDEL 360
DB 316 TYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPSPRDEL 375
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 420
DB 376 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 435
QY 421 QGNVFSCVMHEALHNHYTQKSLSLSPGK 449
DB 436 QGNVFSCVMHEALHNHYTQKSLSLSPGK 464

RESULT 11
US-10-474-832-4
; Sequence 4, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-474-832-4

Query Match 71.7%; Score 2201.5; DB 15; Length 447;
Best Local Similarity 92.9%; Pred. No. 3.6e-132;
Matches 416; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGGGLVQPGGSLRLSAAAGFTFSRYTTSWVRQAPGKGLEWVATISGGGH-TYY 59
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYYFDWSWQOQTTLTVSSA 120
DB 60 LDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYYFDWSWQOQTTLTVSSA 119
QY 121 STKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSSG 180
DB 120 STKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAVLQSSG 179
QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPAPPELLGCP 240
DB 180 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDPKVEPKSCDKTHTTCCPPAPPELLGCP 239
QY 241 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300
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Db 240 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299
QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360
Db 300 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 359
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQ 420
Db 360 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQ 419
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448
Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447

RESULT 12
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

Query Match 71.7%; Score 2200.5; DB 14; Length 444;
Best Local Similarity 92.4%; Pred. No. 4.1e-132;
Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLWVAYISSGSGTY 60
Db 1 EVQLVESGGGLVKPGGSLRLS CAASGFTFSSYDMSWVRQAPAGKLEWVSTISSGGSYTY 60
QY 61 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTTLTVSSA 120
Db 61 LOSIKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARQGL-----DYMGRGTLTVSSA 115
QY 121 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
Db 116 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 175
QY 181 LYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
Db 176 LYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 235
QY 121 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
Db 116 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 175
QY 181 LYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
Db 176 LYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 235
QY 241 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
Db 236 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295
QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360
Db 296 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 355
QY 241 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
Db 236 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295
QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360
Db 296 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 355
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQ 420
Db 356 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQ 415
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 449

Db 416 QGNVFSCSVNHEALHNHYTQKSLSLSPGK 444

RESULT 13
US-10-704-522-6
; Sequence 6, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6

Query Match 71.7%; Score 2200.5; DB 16; Length 444;
Best Local Similarity 92.4%; Pred. No. 4.1e-132;
Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLWVAYISSGSGTY 60
Db 1 EVQLVESGGGLVKPGGSLRLS CAASGFTFSSYDMSWVRQAPAGKLEWVSTISSGGSYTY 60
QY 61 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTTLTVSSA 120
Db 61 LOSIKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARQGL-----DYMGRGTLTVSSA 115
QY 121 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
Db 116 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 175
QY 181 LYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
Db 176 LYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 235
QY 241 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
Db 236 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295
QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360
Db 296 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 355
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQ 420
Db 356 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQ 415
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPGK 449
Db 416 QGNVFSCSVNHEALHNHYTQKSLSLSPGK 444

RESULT 14
US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 32.9571 Seconds
(without alignments)
1699.125 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVSGGDFVKPGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	57.5	330	1 GHU	Ig gamma-1 chain C
2	1630.5	53.1	377	2 A23511	Ig gamma-3 chain C
3	1628.5	53.0	377	2 A60764	Ig gamma-3 chain C
4	1604	52.2	326	1 G2HU	Ig gamma-4 chain C
5	1590.5	51.8	327	1 G4HU	Ig gamma-4 chain C
6	1507.5	49.1	444	2 PC4436	Ig gamma-2 chain C
7	1466	47.7	470	2 S22080	Ig heavy chain pre
8	1430.5	46.6	469	2 S37483	Ig gamma-2a chain
9	1423	46.3	374	2 S69339	Ig heavy chain V r
10	1421	46.3	446	2 S40295	Ig gamma-2a chain
11	1412	46.0	472	2 S31459	Ig gamma-1 chain -
12	1365	44.4	474	1 G2MS11	Ig gamma-2b chain
13	1343.5	43.7	475	2 S01321	Ig gamma-2b chain
14	1263	41.1	328	2 I47159	Ig gamma-2a chain
15	1260	41.0	255	4 S31866	Ig gamma-1 chain C
16	1257	40.9	328	2 I47160	Ig gamma-2b chain
17	1254	40.8	234	2 PT0207	Ig gamma chain C r
18	1231	40.1	328	2 I47158	Ig gamma 1 chain C
19	1230.5	40.1	323	1 GHRB	Ig gamma chain C r
20	1227	40.0	328	2 I47161	Ig gamma 3 chain C
21	1216.5	39.6	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2 C30554	Ig heavy chain C r
23	1152	37.5	326	2 PS0017	Ig gamma-1 chain C
24	1151	37.5	329	1 G3H0W1	Ig gamma-3 heavy c
25	1146.5	37.3	333	2 PS0018	Ig gamma-2b chain
26	1142	37.2	324	1 G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1 G1MSC	Ig gamma-3 chain C
28	1139	37.1	393	1 G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1 G3MSM	Ig gamma-3 chain C

30	1126	36.7	330	1 G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1 G2MSAB	Ig gamma-2a chain
32	1121	36.5	399	1 G2MSAM	Ig gamma-2a chain
33	1118.5	36.4	329	2 S00847	Ig gamma-2c chain
34	1118	36.4	548	2 S38864	Ig epsilon chain C
35	1112	36.2	322	2 PS0019	Ig gamma-2a chain
36	1092.5	35.6	327	2 S06611	Ig gamma-2b chain
37	1082	35.2	405	1 G2MSBM	Ig gamma-2b chain
38	1066	34.7	277	2 I47162	Ig gamma 4 chain c
39	845.5	27.5	549	2 S04845	Ig heavy chain pre
40	817.5	26.6	249	2 S69340	Ig heavy chain VHI
41	802.5	26.1	572	2 B46529	Ig y heavy chain (
42	801.5	26.1	241	2 S69131	Ig heavy chain (DO
43	770	25.1	218	2 A36040	Ig heavy chain V-I
44	760	24.7	220	2 A49444	Ig gamma-1 heavy c
45	744.5	24.2	254	2 B31790	Ig heavy chain V r
46	740.5	24.1	213	2 S68213	Ig heavy chain (Ma
47	734	23.9	246	2 S38950	Ig gamma chain - m
48	731	23.8	627	2 I46883	Ig mu chain precu
49	707	23.0	180	2 I46732	Ig gamma heavy cha
50	695.5	22.6	585	2 A46507	Ig alpha chain - c
51	690	22.5	153	1 ICG12	interleukin-2 prec
52	690	22.5	153	1 ICHU2	interleukin-2 prec
53	686	22.3	220	2 S68211	Ig heavy chain (Ma
54	665.5	21.7	592	2 S25705	Ig mu chain - sh
55	652	21.2	231	2 PC4155	Ig gamma-2b chain
56	648.5	21.1	568	2 A34891	Ig heavy chain pre
57	640	20.8	214	2 PC4202	monoclonal antibod
58	637	20.7	577	2 I50731	Ig heavy chain - n
59	620.5	20.2	221	2 S49220	Ig gamma-1 chain -
60	604	19.7	504	2 S00390	Ig gamma chain (cl
61	587	19.1	509	2 S17597	Ig delta chain (WI
62	573.5	18.7	568	2 A45804	Ig mu chain C regi
63	571	18.6	152	2 S14236	Ig gamma-1 chain C
64	547	17.8	143	2 S25624	Ig heavy chain V r
65	534.5	17.4	154	2 JN0698	interleukin 2 prec
66	534	17.4	342	2 A46529	Ig gamma chain (5.
67	528	17.2	170	2 A35944	Ig gamma-2a chain
68	516.5	16.8	573	2 S12838	Ig mu chain precu
69	509.5	16.6	448	2 S03186	Ig heavy chain C r
70	492	16.0	428	1 EHHU	Ig epsilon chain C
71	490	16.0	97	2 S26652	Ig gamma-1 chain C
72	486	15.8	429	1 EHRT	Ig epsilon-chain -
73	485.5	15.8	426	2 I36948	anti-peptide Fab'
74	482.5	15.7	155	2 S33509	interleukin-2 - Mo
75	479	15.6	119	2 B34353	interleukin-2 prec
76	478.5	15.6	154	2 S16241	Ig heavy chain pre
77	478	15.6	152	2 B26471	Ig heavy chain, se
78	478	15.6	580	2 A46538	Ig heavy chain V r
79	471	15.3	120	2 S55536	Ig heavy chain V r
80	470.5	15.3	121	2 I27887	Ig heavy chain V r
81	469.5	15.3	433	2 S31436	Ig upailon chain -
82	469	15.3	120	2 S55537	Ig heavy chain V r
83	469	15.3	122	2 E27888	Ig heavy chain V r
84	469	15.3	149	2 S31391	interleukin-2 prec
85	467	15.2	111	2 PH1007	Ig heavy chain V r
86	467	15.2	160	2 S05271	Ig heavy chain pre
87	466.5	15.2	118	2 PH0097	Ig heavy chain V r
88	466.5	15.2	119	2 F27888	Ig heavy chain V r
89	464	15.1	138	2 S09258	Ig heavy chain V r
90	463	15.1	120	2 S55539	Ig heavy chain V r
91	462	15.0	117	2 S20641	Ig heavy chain V r
92	461	15.0	117	2 PL0249	Ig heavy chain V r
93	460.5	15.0	118	2 PH0096	Ig heavy chain V r
94	460	15.0	120	2 S55538	Ig heavy chain V r
95	457	14.9	1005	2 T18537	Ig heavy chain - c
96	456	14.8	119	2 S31107	Ig heavy chain - h
97	456	14.8	124	2 C27888	Ig heavy chain V r
98	456	14.8	138	2 S31666	Ig heavy chain V r
99	455.5	14.8	112	2 S26327	Ig heavy chain V r
100	455.5	14.8	147	2 I37780	Ig variable region

ALIGNMENTS

RESULT 1

GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:CROSS-references: UNIPROT:P01857; EMBL:217370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:CROSS-references: EMBL:217370
R:Yatakehashi, N.; Ueda, S.; Obata, M.; Nakai, T.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:CROSS-references: EMBL:217370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primärstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOI; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobi
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:CROSS-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) h
ain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lai
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 57.5%; Score 1767; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.6e-92;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
DB 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPPELPGG 239
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPPELPGG 120
QY 240 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 300 STYRVSVLTVLHDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 359
DB 181 STYRVSVLTVLHDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 419
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
QY 420 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 449
DB 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:CROSS-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
C:Genetics:
A:Gene: GDB:IGHG3
A:CROSS-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33

A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 53.1%; Score 1630.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 1.4e-84;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 120 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQSS 179
DB 1 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQSS 60
QY 180 GLYSLSVVTVPSSSLGTQYIYCNVNHKPSNTKVDKKV----- 217
DB 61 GLYSLSVVTVPSSSLGTQYIYCNVNHKPSNTKVDKKVLTPLGDTTHTCPCRPKSC 120
QY 218 -----BPKSCDKTHTCPCPAPPELLGSPSVFLFPKPOT 252
DB 121 DTPPPCPCRPKSCDTPPPCPCRPKSCDTPPPCPCRPAPELLGSPSVFLFPKPOT 180
QY 253 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPRBEQYNSTYRVVSVLTVLH 312
DB 181 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPRBEQYNSTYRVVSVLTVLH 240
QY 313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 372
DB 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300
QY 373 GYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVSCSVMHE 432
DB 301 GYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVSCSVMHE 360
QY 433 ALHNHYTQKSLSLSPGK 449
DB 361 ALHNRTQKSLSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 53.0%; Score 1628.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 1.9e-84;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 120 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQSS 179
DB 1 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQSS 60
QY 180 GLYSLSVVTVPSSSLGTQYIYCNVNHKPSNTKVDKKV----- 217
DB 61 GLYSLSVVTVPSSSLGTQYIYCNVNHKPSNTKVDKKVLTPLGDTTHTCPCRPKSC 120
QY 218 -----BPKSCDKTHTCPCPAPPELLGSPSVFLFPKPOT 252
DB 121 DTPPPCPCRPKSCDTPPPCPCRPKSCDTPPPCPCRPAPPELLGSPSVFLFPKPOT 180

QY 253 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPRBEQYNSTYRVVSVLTVLH 312
DB 181 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPRBEQYNSTYRVVSVLTVLH 240
QY 313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 372
DB 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300
QY 373 GYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVSCSVMHE 432
DB 301 GYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVSCSVMHE 360
QY 433 ALHNHYTQKSLSLSPGK 449
DB 361 ALHNRTQKSLSLSPGK 377

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; P
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein T11
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707

A;Contents: annotation; Sa, disulfide bonds

C;Genetics:

A;Gene: GDB:IGHG2

A;Cross-references: GDB:119338; OMIM:147110

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into lai

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.2%; Score 1604; DB 1; Length 326;

Best Local Similarity 91.2%; Pred. No. 3.7e-83;

Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

Qy 120 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179

Db 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTPCPAPPELLGG 239

Db 61 GLYSLSSVVTVPSSNFGTQTYTCNVDHPSNTKVDKTKVERKCCVE- --CPCPAPP- VAG 116

Qy 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 299

Db 117 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEOFN 176

Qy 300 STYRVSVSLTVLHVDWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359

Db 177 STFRVSVSLTVLHVDWLNKGEYCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSRDE 236

Qy 360 LTRNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSLKLTVDKSRW 419

Db 237 MTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPPMLDSDGSFPLYSLKLTVDKSRW 296

Qy 420 OQGNVFCSCVMHEALHNHYTKLSLSPGK 449

Db 297 OQGNVFCSCVMHEALHNHYTKLSLSPGK 326

RESULT 5

G4HU

Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004

C;Accession: A90933; A90249; A02150

R;Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933

A;Molecule type: DNA

A;Residues: 1-327 <ELL>

A;Cross-references: UNIPROT:P01861

A;Note: the sequence was determined from the germline gene

R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant h

A;Reference number: A90249; MUID:70207560; PMID:4192699

A;Accession: A90249

A;Molecule type: protein

A;Residues: 1-30;81-326 <PIN>

C;Genetics:

A;Gene: GDB:IGHG4

A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14q32.33-14q32.33

A;Introns: 99/1, 111/1, 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into lai

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.8%; Score 1590.5; DB 1; Length 327;

Best Local Similarity 90.9%; Pred. No. 2.1e-82;

Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

Qy 120 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179

Db 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTPCPAPPELLGG 239

Db 61 GLYSLSSVVTVPSSSLGTQTYTCNVDHPSNTKVDKRVESK- --YGPCCPCPAPPELLGG 117

Qy 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 299

Db 118 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEOFN 177

Qy 300 STYRVSVSLTVLHVDWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359

Db 178 STYRVSVSLTVLHVDWLNKGEYCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy 360 LTRNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSLKLTVDKSRW 419

Db 238 MTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSLKLTVDKSRW 297

Qy 420 OQGNVFCSCVMHEALHNHYTKLSLSPGK 449

Db 298 QEGNVFCSCVMHEALHNHYTKLSLSPGK 327

RESULT 6

PC4436

monoclonal antibody 13-1 heavy chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C;Accession: PC4436

R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin

A;Reference number: JC5810; MUID:98063277; PMID:9398605

A;Accession: PC4436

A;Molecule type: protein

A;Residues: 1-444 <AKA>

C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed agains

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IMM>

F:22/Disulfide bonds: interchain (to 98) #status predicted

F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 49.1%; Score 1507.5; DB 2; Length 444;

Best Local Similarity 60.9%; Pred. No. 1.4e-77;

Matches 276; Conservative 74; Mismatches 90; Indels 13; Gaps 6;

Qy 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFSAHYAMSWRQTQPAKRLWYAYIS- --SGSGGT 58

Db 1 EVQXVETGGGLVRFQNSLKLSCLTSGFTFSNYRMHWLQPPGKRLWIAVITKSDNYGA 60

Qy 59 YYSDSVKGRTTISRDNKNTLYLQWRSLSRSDSAMYFCTRVLKLTGYTFDSGQGTTLTVS 118

Db 61 KYAESVGRFTISRDDSKSSVYLQWNLRLREEDTATYYCCRTTP- WYIAMDQCGQGTTSVVS 119

Db 438 NWVERNSYSCSVVHGLHHHTTKFSRTPGK 469

RESULT 9

S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 46.3%; Score 1423; DB 2; Length 374;
Best Local Similarity 61.9%; Pred. No. 6.4e-73;
Matches 281; Conservative 23; Mismatches 46; Indels 104; Gaps 4;

Qy	1	EVTLVESGGDFVKPGSLKVS	CAAGFAPSH--YAMSVWRQTPAKRL	EWAYISSGGSGT	58		
Db	20	QITLKESGPTLVKQTTLT	LTCTFSGFLSKSGVGVMI	ROPQGALEWLALI-FWDDDK	78		
Qy	59	YVSDSVKGRFTISRDN	AKNTLYLQWRLSRSDS	AMVFCFTRVKLG---	TYVFDMSGQGTLL	115	
Db	79	RYSPLRLTLITKDT	SKNQVLLTMNVDPA	TATYYCGYSEVGGQGYR	FHSMGQGTLLV	138	
Qy	116	TVSSASTKGPSVF	FLAPSSKSTSGGTAAL	GLCLVKDYFPEPVT	VSWSNGALTSGVHTFP	175	
Db	139	TVSS-----	-----	-----	-----	142	
Qy	176	LOSSGLYSLSSVV	VPSSSLGTQYICNVN	HKPSNTKVDKVPK	SCDKTKTCCPCPAPE	235	
Db	143	-----	-----	-----	EPKSCDKTKTCCPCPAPE	160	
Qy	236	LLGGPSVFLFP	PKPXTLMI	SRTPEVTCVVVDV	SHEDPEVKFNWVVDG	VEVHNAKTKPRE	295
Db	161	LLGGPSVFLFP	PKPXTLMI	SRTPEVTCVVVDV	SHEDPEVKFNWVVDG	VEVHNAKTKPRE	220
Qy	296	EQYNSTYRVSV	VLTVLHQD	WLNKGEYKCKVSN	KALPAPIEKTISKAK	QPREPQVYTLPP	355
Db	221	EQYNSTYRVSV	VLTVLHQD	WLNKGEYKCKVSN	KALPAPIEKTISKAK	QPREPQVYTLPP	280
Qy	356	SRDELTQNQV	SLTCLVKGF	PSDIAVEWESNGQP	ENNYKTPPVLDS	DGSGFFLYSKLTVD	415
Db	281	SREEMTKNQV	SLTCLVKGF	PSDIAVEWESNGQP	ENNYKTPPVLDS	DGSGFFLYSKLTVD	340
Qy	416	KSRWQGNV	FSCSVMH	EALHNHYTK	SLSPGK	449	
Db	341	KSRWQGNV	FSCSVMH	EALHNHYTK	SLSPGK	374	

RESULT 10

S40295
Ig gamma-2a chain (mab735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Prosch, M.; Weisgerber, C.; B
submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
A:Cross-references: UNIPROT:Q99L25
C:Genetics:

A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CHI>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 46.3%; Score 1421; DB 2; Length 446;
Best Local Similarity 58.7%; Pred. No. 1e-72;
Matches 264; Conservative 71; Mismatches 109; Indels 6; Gaps 4;

Qy	1	EVTLVESGGDFVKPGSLKVS	CAAGFAPSHYAMSVWRQTPAKRL	EWAYISSGGSGTY	60			
Db	1	QIQLOQSGPELV	PGASVKISCKASGVTFTDYI	HWVKQRPGEGLWGIY	PGSGNTKY	60		
Qy	61	SDSVKGRFTISRDN	AKNTLYLQWRLSRSDS	AMVFCFTRVKLTGY	YFDSMGOGTLLTVSSA	120		
Db	61	NEKFKGKATL	TVDTSSTAYMQLS	SLTSDSAVYFCARG--	GKFAMDYWGOGTS	VTVSSA	118	
Qy	121	STKGPSVF	FLAPSSKSTSGGTAAL	GLCLVKDYFPEPVT	VSWSNGALTSGVHTFP	AVLQSSG	180	
Db	119	KTTAPSV	VFLAPVCGDTTGSSV	TGCLVKGFPEPVL	TWNSGSLSSGSHV	TFPAVLQSD-	177	
Qy	181	LYSLSSVV	TVPSSSLGTQYICNVN	HKPSNTKVDKVPK	SCDKTKTHTCP--	CPAPELLG	238	
Db	178	LYTLSSSV	TVTSTWPSQSITCN	VAPASSTKVDKDKI	EPRG-PTIKPCPPCK	CPAPNLLG	236	
Qy	239	GPSVFL	PPPKDITLMI	SRTPEVTCVVVDV	SHEDPEVKFNWVVDG	VEVHNAKTKPRE	298	
Db	237	GPSVFI	PPPKIDVLMISL	SPMVTVCVVVDV	SEDDPDQISW	FVNNVEVLTAQTQ	THREDY	296
Qy	299	NSTYRV	SVSLTVLHQD	WLNKGEYKCKVSN	KALPAPIEKTISKAK	QPREPQVYTLPP	358	
Db	297	NSTYRV	SVSLPIQHOD	WMSGKEFKCKVNN	KDLPAPIERTISKPG	SVRAPQVYVLP	PPPEE	356
Qy	359	ELTKNQV	SLTCLVKGF	PSDIAVEWESNGQP	ENNYKTPPVLDS	DGSGFFLYSKLTVD	KSR	418
Db	357	EMTKQV	TLLTCMTWDF	MPEDIYVEWTN	NGKTELNYKTELP	VDSDSGSYFMY	SKLAVEKKN	416
Qy	419	WQGNV	FSCSVMH	EALHNHYTK	SLSPG	448		
Db	417	WVERNSY	SCSVVH	EGLHNHHTTK	SFSRTPG	446		

RESULT 11

S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patric, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459
A:Accession: S31459
A:Status: preliminary
A:Molecule type: mRNA

A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

Query Match 46.0%; Score 1412; DB 2; Length 472;
Best Local Similarity 58.4%; Pred. No. 3.5e-72;
Matches 269; Conservative 66; Mismatches 108; Indels 18; Gaps 5;

Qy 1 EVTLVESGGDFVKPGGSLKVCSCAASGFAPSHYAMSWRQTPAKRLWVAYISSGGSG---57
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
18 QVRLOESGPSLATLLQLTSLTCTTSGLNNGYDWRQAPGKALEWL-----GSGSYDE 72
Qy 58 -TTYSDSVKGRFTISRDNAXNTLYLMRSIARSEDAMFYCTRVLKLTGY-----FDSWG 110
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
73 DIDYNPLVKSRLSITKTDSKSQVSLTSTVTDTAVYCARVDYDSSHAFVASYDFWG 132
Qy 111 QGITLTLYSSASTKGPSVFPLAPSSEKTSISGGTAAGCLVKDYFEPEPVTVSNSGALTSGVH 170
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
133 PGLLIIVLSASTTPPKVPYLPITSCCGDTSSTSVTLGCLVSSSYMPEFPVTWN SGALTSGVH 192
Qy 171 TFPVAVLQSSGLYSLVSVVTVSPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230
Db 193 TFPAILQSSGLYSLVSVVTVSPASTSGAQTFICNAHPASSTKVDKRVGPCDPCKHC-R 251
Qy 231 CPAPELLGSPSFVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVGEVHNAK 290
Db 252 CPPPELGSPSFVIFPPKPDKDLTISGTPETVCVVVDVGQDDPEVQFSWFVDNVEVRTAR 311
Qy 291 TKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPRPQV 350
Db 312 TKPREEOFNSTRVVSALPQHODWTGCKEKFKCVNEALPAPIVTRTISRITKGAAREPQV 371
Qy 351 YTLPPSDELTKNOVSLTCLVKGPYSDIAVENESGOP--ENNYKTTTPVLSDSGSFEL 408
Db 372 YVLAPPQEEUSKSTLSLTVLGTGPDYIAVEWKNGQPESSEDKYITTSQLDADGSYFL 431
Qy 409 YSKLTVDKSRWQQGNVPCSMHEALHHYTKQSLSLSPGK 449
Db 432 YSRLRVNDKSNQEGDITACVVMHEALHHYTKQSISKPPGK 472

RESULT 12
G2MS11
IG gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text change 09-Jul-2004
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
Submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A;Reference number: S25057
A;Accession: S25057
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAAA7649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A:Molecule type: DNA
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: The sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11

A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TUI>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A:Cross-references: GB:J00461
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967
A:Accession: A53598
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
A:Comment: The a allele sequence is shown.
C:Genetics:
A:Introns: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGH, the subunits associate into larger superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F;157-222/Domain: immunoglobulin homology <IM1>
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220,288-348,394-452/Disulfide bonds: #status predicted
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.4%; Score 1365; DB 1; Length 474;
Beat Local Similarity 55.8%; Pred. No. 1.6e-69;
Matches 256; Conservative 72; Mismatches 117; Indels 14; Gaps 4;

Qy	1	EVTLVESGGDFVKPGGSLKVS CAASGAFASHYAMSWVRQTTPAKRLIEWAYISSGGSGTY 60
Db	20	EVQLQQSGPELVNPGASVKMSCKASGYTFITVVMHWVKQKPGQGLEWIGYINPNKDGTKF 79
Qy	61	SDSVKGRFTISRDAKNTLYLQMSSLRSDESNYFECTRVKLTGY---YFDSNGQGTTLTV 117
Db	80	NEKPKGKATLTSKSSNTAYMELSSLTSEDSAVYYCAR---DYDYDMFAYWGQGLTVT 135
Qy	118	SSAGTKGSPVPLAPSSKSTSGGTAALCLVKDYKPPETVTVSNWGALTSGVHTPFAVLQ 177
Db	136	SAAKTTPSPVPLAPGCGDTTGSSVTSCLVKGPFPESVTVTVNWSGSLSSVHTLSQALL 195
Qy	178	SSGLYSLSSVVTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVKPKSCDKT-HTCPP----- 230
Db	196	QSGLYTWSSSVTVPPSSVTPSQVTCVAHPASSTTVDKLEPSPGPISTINPCPKCECHK 255
Qy	231	CPAPELLGGSPVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVKFKNWYDGVVHNAK 290
Db	256	CPAPNLEGGSPVFIPFPNKKDVLMI SLTPKVTTCVVDVSEDDPDVQISFNVNNEVHTAQ 315
Qy	291	TKPREEOYNSTYRVSVLTVLHQDNLGKCYKCKVSKNALPAPIETKTIISKAKGQPREPV 350
Db	316	TQTHREDYNSTIRVSVLTPLTQHQDMMGSKFPCKVNNKDLPSPIERTISKIKGLVRAPQ 375
Qy	351	YTLPPSRDELTKQVSLTCLVKGFYPSPDIAVWEWSNGQFENNYKTTPTPVLDSDGSGFFLYS 410

Db 376 YILPPAQLSKDVSILCLVGFNPGDISVWTSNGHTENYKDTAPVLSDSGSYFIYS 435
QY 411 KLTVDKSRWQGNVPSVCSVMHEALHNHYTKSLSLSPGK 449
Db 436 KLNMTSKWEKTDSPSCNVRHEGLKNYLYLKKTISSPGK 474

RESULT 13
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed at
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: This sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 43.7%; Score 1343.5; DB 2; Length 475;
Best Local Similarity 55.4%; Pred. No. 2.5e-68;
Matches 253; Conservative 75; Mismatches 120; Indels 9; Gaps 4;

QY 1 EVTLVESGDFVKPGGSLKVS CAASGPAFASHYAMSVRQTAKRLWVAYISSGSGTY 60
Db 20 QVOLQSGAELARP GASVKLSCKASGYLTLSYGISWVKQRTQGLEWIGEIVPGSGSYF 79
QY 61 SDSVKGRTISRDNAKNTLYLQMRSLRSEDSNMYECTRVK-LGTYYPDSWGQGTLLTVSS 119
Db 80 NEKPKGKATLTVDKSSSTAYLHLSLSLTSEDSAVYFCAGPRQVGLLPFGYWGQGLTVLTASA 139
QY 120 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db 140 AKTTPSVYPLAPGCDITGSSVTLGCLVKGYFPEPVTVSWNSGSLSSVHTFPAQLQ-S 198
QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKT-HTCPP-----CP 232
Db 199 GLYTMSSSVTPSSRWPSQTVCVAHPASSTTVDBKLEPSGPTSTINPCPPCKECKCP 258
QY 233 APGLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 292
Db 259 APNLEGGPSVFIFPPNIKDVLMSLTPTKVTCTVVDVSEDDPDVQISWFNWVNVLTATQ 318
QY 293 PREEQYNSTYRVSVLTVLHODWLGKSKYKCVSNKALPAPIEKTISKAKGQPREPQVY 352
Db 319 THREDYNTIRVVSALPTQHQDMWGSEKFKCKVNNKDLPAPIERTISKIGIVRAPQYI 378
QY 353 LPPSRDELTKNQVSTCLVKGYFSPDIAVEWESNQPNNTKTPPVLDSDGSPFLYSKL 412
Db 379 LSPPEQLSRKDVSLTCLAVGSPEDISVEMTSNGHTENYKDTAPVLSDSGSYFIYSKL 438
QY 413 TVDKSRWQGNVPSVCSVMHEALHNHYTKSLSLSPGK 449
Db 439 NMKTSKWEKTDSPSCNVRHEGLKNYLYLKKTISSPGK 475

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kaczkovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IGG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 1263; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 5.3e-64;
Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;

QY 120 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db 1 AKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVSWNSGSLSSGVHTFPAVLQPS 60
QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 239
Db 61 GLYSLSVVTVPASSLSKSYTCNVNHPATTTKVDKRVGKTGKPPCPICPACESP----G 116
QY 240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299
Db 117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 176
QY 300 STYRVSVLTVLHODWLGKSKYKCVSNKALPAPIEKTISKAKGQPREPQVYTPPPSDE 359
Db 177 STYRVSVLTVLHODWLGKSKYKCVSNKALPAPIEKTISKAKGQPREPQVYTPPPHAE 236
QY 360 LTKNQVSTCLVKGYFSPDIAVEWESNQ--PENNYKTTPPVLDSDGSPFLYSKLTVDKS 417
Db 237 LSRKSVSTCLVIGFYPPDIDVEMQNGQPEPEGNRYRTTPQDVGDTGYFLYSKFSVDKA 296
QY 418 RWQGNVPSVCSVMHEALHNHYTKSLSLSPGK 449
Db 297 SWQGGIFQCAVMHEALHNHYTKSLSLSPGK 328

RESULT 15
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 41.0%; Score 1260; DB 4; Length 255;
Best Local Similarity 97.5%; Pred. No. 5.8e-64;
Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 211 TKVDKVEPKSCDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 270
Db 17 TVAQADVESKCDKTHCTCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76
QY 271 EDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLGKSKYKCVSNKAL 330
Db 77 EDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLGKSKYKCVSNKAL 136

Qy	331	PAPIEKTISKAKGQPREPQVYTTLPQSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE	390
Db	137	PAPIEKTISKAKGQPREPQVYTTLPQSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE	196
Qy	391	NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	449
Db	197	NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	255

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Job time : 34.9571 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 151.023 Seconds
(without alignments)
1973.408 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVSGGDFVKGSLKV.....IVEFLNRWTFQCSIIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2184	71.1	470	2 Q6PJA4	Q6pja4 homo sapien
2	2184	71.1	478	2 Q6PI81	Q6pi81 homo sapien
3	2166.5	70.5	475	2 Q6MZQ6	Q6mzq6 homo sapien
4	2160	70.3	472	2 Q6N089	Q6n089 homo sapien
5	2157.5	70.3	475	2 Q6GMW7	Q6gmw7 homo sapien
6	2152.5	70.1	473	2 Q6MZV7	Q6mzv7 homo sapien
7	2146	69.9	480	2 Q6N094	Q6n094 homo sapien
8	2145	69.8	466	2 Q6IN78	Q6in78 homo sapien
9	2140.5	69.7	544	2 Q6PJ95	Q6pj95 homo sapien
10	2126	69.2	466	2 Q6N096	Q6n096 homo sapien
11	2124.5	69.2	473	2 Q6P055	Q6p055 homo sapien
12	2124	69.2	470	2 Q7Z5W1	Q7z5w1 homo sapien
13	2111	68.7	482	2 Q7Z351	Q7z351 homo sapien
14	2080.5	67.7	481	2 Q6N097	Q6n097 homo sapien
15	2066.5	67.3	469	2 Q7Z7P5	Q7z7p5 homo sapien
16	2052.5	66.8	475	2 Q6N095	Q6n095 homo sapien
17	2037	66.3	476	2 Q6GMX1	Q6gmx1 homo sapien
18	2027.5	66.0	465	2 Q6GMX6	Q6gmx6 homo sapien
19	2026	66.0	480	2 Q6PJF1	Q6pjf1 homo sapien
20	2018.5	65.7	465	2 Q6P6C4	Q6p6c4 homo sapien
21	2014	65.6	464	2 Q6MZU6	Q6mzu6 homo sapien
22	1957.5	63.7	521	2 Q8N4Y9	Q8n4y9 homo sapien
23	1956	63.7	518	2 Q6N030	Q6n030 homo sapien
24	1939	63.1	493	2 Q68CN4	Q68cn4 homo sapien
25	1916	62.4	417	2 Q6N093	Q6n093 homo sapien
26	1824	59.4	348	2 Q6PYX1	Q6pyx1 homo sapien
27	1812	59.0	473	2 Q8TC63	Q8tc63 homo sapien
28	1790.5	58.3	476	2 Q6MZX7	Q6mzx7 homo sapien
29	1767	57.5	330	1 GC1_HUMAN	GC1_HUMAN
30	1622.5	52.8	509	2 Q8NF17	Q8nf17 homo sapien
31	1604	52.2	326	1 GC2_HUMAN	GC2_HUMAN

32	1590.5	51.8	327	1 GC4_HUMAN	P01861 homo sapien
33	1535.5	50.0	487	2 Q65ZL2	Q65zl2 mus ap. fv/
34	1527.5	49.7	473	2 Q91Z05	Q91z05 mus musculu
35	1524.5	49.6	354	2 Q86TT2	Q86tt2 homo sapien
36	1521.5	49.5	471	2 Q68K04	Q68k04 mus musculu
37	1509	49.1	458	2 Q65ZQ1	Q65zq1 homo sapien
38	1484	48.3	464	2 Q6FIP8	Q6fip8 mus musculu
39	1456.5	47.4	473	2 Q9D8L4	Q9d8l4 mus musculu
40	1455.5	47.4	463	2 Q99LC4	Q99lc4 mus musculu
41	1454	47.3	470	2 Q7TMK1	Q7tmk1 mus musculu
42	1447	47.1	472	2 Q6PJA7	Q6pja7 mus musculu
43	1442.5	47.0	465	2 Q6FJB2	Q6fjb2 mus musculu
44	1419	46.2	464	2 Q6PF95	Q6pf95 mus musculu
45	1399	45.6	474	2 Q8R3H6	Q8r3h6 mus musculu
46	1266.5	41.2	337	2 Q95M34	Q95m34 equus cabal
47	1264	41.2	679	2 Q96P08	Q96p08 homo sapien
48	1230.5	40.1	323	1 GC_RABIT	P01870 oryctolagus
49	1216.5	39.6	329	1 GC3_CAVPO	P01862 cavia porce
50	1156	37.6	290	1 GC1_HUMAN	P01860 homo sapien
51	1152	37.5	326	1 GCI_RAT	P20759 rattus norv
52	1146.5	37.3	333	1 GCB_RAT	P20761 rattus norv
53	1142	37.2	324	1 GCI_MOUSE	P01868 mus musculu
54	1141	37.2	329	1 GC3_MOUSE	P22436 mus musculu
55	1139	37.1	393	1 GC1M_MOUSE	P01869 mus musculu
56	1130	36.8	398	1 GC3M_MOUSE	P03387 mus musculu
57	1126	36.7	330	1 GCAA_MOUSE	P01863 mus musculu
58	1123.5	36.6	335	1 GCAB_MOUSE	P01864 mus musculu
59	1121	36.5	399	1 GCAM_MOUSE	P01865 mus musculu
60	1118.5	36.4	329	1 GCC_RAT	P20762 rattus norv
61	1112	36.2	322	1 GCA_RAT	P20760 rattus norv
62	1087	35.4	336	1 GCB_MOUSE	P01866 mus musculu
63	1082	35.2	405	1 GCBM_MOUSE	P01867 mus musculu
64	877.5	28.6	606	2 Q6GMV2	Q6gmv2 homo sapien
65	856	27.9	597	2 Q96BB9	Q96bb9 homo sapien
66	849.5	27.7	584	2 Q6LNM3	Q6lnm3 xenopus lae
67	847	27.6	613	2 Q8WUK1	Q8wuk1 homo sapien
68	842	27.4	487	2 Q99KA4	Q99ka4 mus musculu
69	834.5	27.2	303	2 Q6KAM2	Q6kam2 mus musculu
70	828.5	27.0	486	2 Q91Z07	Q91z07 mus musculu
71	816	26.6	585	2 Q6GPX4	Q6gp4 xenopus lae
72	807	26.3	479	2 Q91WP5	Q91wp5 mus musculu
73	799	26.0	493	2 Q6GMX2	Q6gmx2 homo sapien
74	793.5	25.8	494	2 Q96K68	Q96k68 homo sapien
75	788	25.7	593	2 Q6INM5	Q6inm5 xenopus lae
76	787	25.6	614	2 Q6DDQ7	Q6ddq7 xenopus lae
77	785	25.6	480	2 Q91XE1	Q91xe1 mus musculu
78	783	25.5	485	2 Q6PDB8	Q6pdb8 mus musculu
79	781	25.4	499	2 Q8N5K4	Q8n5k4 homo sapien
80	776	25.3	493	2 Q8NCL6	Q8nc16 homo sapien
81	772	25.1	479	2 Q6MZV6	Q6mzv6 homo sapien
82	768	25.0	487	2 Q6ZVX0	Q6zvx0 homo sapien
83	753.5	24.5	494	2 Q8ZW64	Q8zw64 homo sapien
84	749	24.4	483	2 Q8MZX9	Q8mzx9 homo sapien
85	748.5	24.4	484	2 Q8VEA0	Q8vea0 mus musculu
86	748	24.4	487	2 Q8OZ17	Q8oz17 mus musculu
87	747	24.3	613	2 Q8VCX7	Q8vcx7 mus musculu
88	737	24.0	519	2 Q6N092	Q6n092 homo sapien
89	731.5	23.8	614	2 Q7TMT6	Q7tmt6 mus musculu
90	709	23.1	597	2 Q6GMX5	Q6gmx5 homo sapien
91	709	23.1	597	2 Q9BU10	Q9bu10 homo sapien
92	703	22.9	498	2 Q6N041	Q6n041 homo sapien
93	703	22.9	597	2 Q9BQB8	Q9bqb8 homo sapien
94	697.5	22.7	595	2 Q8WUX4	Q8wux4 homo sapien
95	697.5	22.7	625	2 Q96AA6	Q96aa6 homo sapien
96	690.5	22.5	500	2 Q6N091	Q6n091 homo sapien
97	690	22.5	153	1 IL2_HUMAN	P60568 homo sapien
98	690	22.5	153	1 IL2_HYLLA	P60569 hylobates l
99	690	22.5	153	2 Q6NZ93	Q6nz93 homo sapien
100	687.5	22.4	500	2 Q9BRV0	Q9brv0 homo sapien

ALIGNMENTS

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RESULT 1
Q6FJA4 PRELIMINARY; PRT; 470 AA.
AC Q6FJA4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL; BC018747; AAH18747.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match
Best Local Similarity 91.4%; Pred. No. 1.2e-131;
Matches 412; Conservative 10; Mismatches 27; Indels 2; Gaps 1;

QY 1 EYTLVESGDFVYKPGSLKVCASGAPFASHYMSWVRQTAKRLWVAYISSGSGTY 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EVQLVESGGLVQPGSLRLSCVSGFTFSSYMSWVRQAPGKGLEWVANIQDGSERY 79
QY 61 SDSVKGRTTISRDNAKNTLYLQMSLRSDSNMYECTRVKLTGY---YDSWCGQTLTVS 118
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 VDSVKGRTTISRDNAKNTLYLQMSLRSDSNMYECTRVKLTGY---YDSWCGQTLTVS 139
QY 119 SASTKGPVFPPLAPSSKTSKSTGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQS 178
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 140 SASTKGPVFPPLAPSSKTSKSTGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQS 199
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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 71.1%; Score 2184; DB 2; Length 478;
Best Local Similarity 90.0%; Pred. No. 1.2e-131;
Matches 413; Conservative 13; Mismatches 23; Indels 10; Gaps 2;

QY 1 EVTLVESGGDFVFKPGGSLKVSACASGFASFHYAMSVVRQTPAKLEWVAIVISSGGSGTYY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVESGGGLVQPGGSLRLSCLASGFTFSYMSWVRQAPGKLEWVAIKDGSKKYY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYFCTR-----VKLGTYTF--DSWG 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 VDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYFCTR-----VKLGTYTF--DSWG 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 111 QGTTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 140 KGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 171 TPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKNTKYDKKVPKSCDKTHTCPP 230
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 200 TPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKNTKYDKKVPKSCDKTHTCPP 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 231 CPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 290
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 260 CPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 319
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 291 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 320 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 351 YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFELY 410
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 380 YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFELY 439
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 411 KLTVDKSRWQQGNVFCSVNHEALHNHYTQKSLSLSPGK 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 440 KLTVDKSRWQQGNVFCSVNHEALHNHYTQKSLSLSPGK 478
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human CDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.

RESULT 4
Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
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DR SMART: SM00406; IGV: 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
Query Match 70.3%; Score 2160; DB 2; Length 472;
Best Local Similarity 89.9%; Pred. No. 4.1e-130;
Matches 408; Conservative 16; Mismatches 24; Indels 6; Gaps 3;
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFHYAMSWVRQTAKRLIEWAYISSGGSGTY 60
DB 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTDDYAMEHWVRQAPGKGLWVSGISWSSGSIAY 79
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTG---YYF--DSWGGTTL 115
DB 80 ADSVKGRTTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTG---YYF--DSWGGTTL 138
QY 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
DB 139 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 198
QY 176 LQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPE 235
DB 199 LQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPE 258
QY 236 LLGGPSVFLFPPPKKDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
DB 259 LLGGPSVFLFPPPKKDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 318
QY 296 EQYNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGPREPVQVYTLPP 355
DB 319 EQYNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGPREPVQVYTLPP 378
QY 356 SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 415
DB 379 SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 438
QY 416 KSRWQOGNVFSCVSMHEALHNHYTQKSLSLSPGK 449
DB 439 KSRWQOGNVFSCVSMHEALHNHYTQKSLSLSPGK 472
RESULT 5
Q6GMW7 PRELIMINARY; PRT; 475 AA.
ID Q6GMW7
AC Q6GMW7
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S., Wang J., Wang J., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.M., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1F55D736860F8 CRC64;
Query Match 70.3%; Score 2157.5; DB 2; Length 475;
Best Local Similarity 89.5%; Pred. No. 6e-130;
Matches 408; Conservative 15; Mismatches 26; Indels 7; Gaps 2;
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFHYAMSWVRQTAKRLIEWAYISSGGSGTY 60
DB 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTDDYAMEHWVRQAPGKGLWVSGISWSSGSIAY 79
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRSEDSAMFYCTRVK-----LGTYY--FDSWGGT 113
DB 80 ADSVKGRTTISRDNKNTLYLQMRSLRSEDSAMFYCTRVK-----LGTYY--FDSWGGT 139
QY 114 TLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
DB 140 TLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199
QY 174 AVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPA 233
DB 200 AVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPA 259
QY 234 PELLGGPSVFLFPPPKKDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
DB 260 PELLGGPSVFLFPPPKKDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319
QY 294 REEQYNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGPREPVQVYTL 353
DB 320 REEQYNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGPREPVQVYTL 379
QY 354 PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 413
DB 380 PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 439
QY 414 VDKSRWQOGNVFSCVSMHEALHNHYTQKSLSLSPGK 449
DB 440 VDKSRWQOGNVFSCVSMHEALHNHYTQKSLSLSPGK 475
RESULT 6
Q6MZV7 PRELIMINARY; PRT; 473 AA.
ID Q6MZV7
AC Q6MZV7
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;


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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGv; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476BAE4C0BFCA47 CRC64;

Query Match 70.1%; Score 2152.5; DB 2; Length 473;
Best Local Similarity 88.3%; Pred. No. 1.3e-129;
Matches 401; Conservative 24; Mismatches 24; Indels 5; Gaps 1;

QY 1 EVTLVSGGDFVKPGGSLKVSACASGFAPFASHYAMSVWROTPAKRLWVAVYISSGGSGTY 60
DB 20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSFENWVRQAPGKLEWLSITRSGNTVY 79
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLT-----YFDSNGQTTL 115
DB 80 ADSLQGRFTISRDNARNSLYLQMRSLRSDSAMYFCTRVKLT-----YFDSNGQTTL 139
QY 116 TVSSASTKGPSVFLPAPSSKTSAGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAV 175
DB 140 TVSSASTKGPSVFLPAPSSKTSAGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAV 199
QY 176 LQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAPE 235
DB 200 LQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAPE 259
QY 236 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPRE 295
DB 260 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPRE 319
QY 296 EQYNSTRVVSIVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPP 355
DB 320 EQYNSTRVVSIVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPP 379
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 415
DB 380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 439
QY 416 KSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 449
DB 440 KSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 473

RESULT 7
Q6N094
ID Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFp686O01196.
GN Name=DKFp686O01196;
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640822; CAB45776.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGv; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 69.9%; Score 2146; DB 2; Length 480;
Best Local Similarity 87.4%; Pred. No. 3.3e-129;
Matches 403; Conservative 19; Mismatches 27; Indels 12; Gaps 1;

QY 1 EVTLVSGGDFVKPGGSLKVSACASGFAPFASHYAMSVWROTPAKRLWVAVYISSGGSGTY 60
DB 20 EEBLVESGGGLVKPGGSLRLSCAASGFTFRSFMNWRQAPGKLEWIAIINSRGNEKY 79
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSDSAMYFCTRVK-----LGTYTFDS 108
DB 80 GESVKGRTISRDNADNSLFLQMRSLRSDSAMYFCTRVK-----LGTYTFDS 139
QY 109 WGGTTLTVSSASTKGPSVFLPAPSSKTSAGTAALGCLVKDYFPEPTVSWNSGALTSG 168
DB 140 WGGTTLTVSSASTKGPSVFLPAPSSKTSAGTAALGCLVKDYFPEPTVSWNSGALTSG 199
QY 169 VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTC 228
DB 200 VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTC 259
QY 229 PPCAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288
DB 260 PPCAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319
QY 289 AKTKPREQYNSTRVVSIVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 348
DB 320 AKTKPREQYNSTRVVSIVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 379
QY 349 QVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFL 408
DB 380 QVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFL 439
QY 409 YSKLTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 449
DB 440 YSKLTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 480

RESULT 8
Q6IN78
ID Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN Name=IGHG1;
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -;
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDE81076E CRC64;

Query Match 69.8%; Score 2145; DB 2; Length 466;
Best Local Similarity 90.0%; Pred. No. 3.7e-129;
Matches 406; Conservative 15; Mismatches 24; Indels 6; Gaps 3;

QY 1 EVTLVSGGDFVKPGSLKVSACAAGFAPSHYAMSVRQTAPKRLWNAVYISGGSGTY 60
DB 20 EVQLVESGGGLIQPGSGLTSLCAASGLTVSSNVMHWVRQAPGKLEWVSLYIGCA-TY 78

QY 61 SDSVGRFTISRDNAKNTLYLQWRSLSRSDSAMFYCTRVLKLTGYTYPDS--WQGGTTLTVS 118
DB 79 ADSVGRFTISRDNSKNTLYLQWNSLRDAEDTAVYICAR---GNYYVPAAPWQGGTLTVTS 135

QY 119 SASTGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 178
DB 136 SASTGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 195

QY 179 SGLYSLSSVTVTPSSSLGQTQYICNVNHPKSTKVDKVEPKSCDKHTCTCPCPAPELIG 238
DB 196 SGLYSLSSVTVTPSSSLGQTQYICNVNHPKSTKVDKVEPKSCDKHTCTCPCPAPELIG 255

QY 239 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDDEPKFNWYVDGVEVNAKTKPREQY 298
DB 256 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDDEPKFNWYVDGVEVNAKTKPREQY 315

QY 299 NSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKISKAKGQPREPPVYTLLPPSRD 358

Db 316 NSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKISKAKGQPREPPVYTLLPPSRD 375
QY 359 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFSLYSLKLTVDKSR 418
Db 376 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFSLYSLKLTVDKSR 435

QY 419 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
Db 436 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466

RESULT 9
Q6PJ95 PRELIMINARY; PRT; 544 AA.
ID Q6PJ95
AC Q6PJ95;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -;
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 1895814B2297C668 CRC64;

Query Match 69.7%; Score 2140.5; DB 2; Length 544;
Best Local Similarity 85.6%; Pred. No. 8.9e-129;
Matches 409; Conservative 16; Mismatches 34; Indels 19; Gaps 2;

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Qy 1 EVTLVSGGDFVFKPGGSLKVS CAASGFAPFASHYAMSVWRQTPAKRLWVAYISSGGSGTTY 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 QAQLVSGGGVVPQGGSLRLS CAASGFRFSNYGMHVROAPKGLWVAVFSYDESCKYY 79
Qy 61 SDSVKGRFTTISRDNKNTLYLQMSLSRSED SAMYFCTRVKLGTY-----YFDSWGQGT 113
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
80 AASVKGRFTTISRDNKNTLSLQMSLSRVEDTAVYYCAKQDPWYSNWFNTNFDWSGRGT 139
Qy 114 TLTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFP 173
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
140 LVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFP 199
Qy 174 AVLOSSGLYSSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHCPPCPA 233
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
200 AVLOSSGLYSSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHCPPCPA 259
Qy 234 PELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKP 293
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
260 PELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKP 319
Qy 294 REEQYNTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
320 REEQYNTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379
Qy 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLT 413
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLT 439
Qy 414 VDKSRWQGNVFCVSNVHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDIQ 471
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
440 VDKSRWQGNVFCVSNVHEALHNHYTQKSLSLSP-----ELQLEESCAEAQ 485
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RESULT 10

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Q6N096 ID Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686i15196;
GN Name=DKFZp686i15196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB45774.1;
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;
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Query Match 69.2%; Score 2126; DB 2; Length 466;
Best Local Similarity 89.3%; Pred. No. 6.1e-128;
Matches 401; Conservative 17; Mismatches 29; Indels 2; Gaps 1;

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Qy 1 EVTLVSGGDFVFKPGGSLKVS CAASGFAPFASHYAMSVWRQTPAKRLWVAYISSGGSGTTY 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 EVTLVSGGGVLPQGGSLKLS CAASGFTVNNYMHVRQAPKGLVWVSLMRDDASEYAT 79
Qy 61 SDSVKGRFTTISRDNKNTLYLQMSLSRSED SAMYFCTRVKLGTYYPDSWGQGTTLTVSSA 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
80 AEFVQGRFTTISRDNKNTLFQLSSLRAREDVAVYYCARGGGFN--FDQWQGTTLTVSSA 137
Qy 121 STKGPSVFPLAPSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQSSG 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
138 STKGPSVFPLAPSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQSSG 197
Qy 181 LYSLSVTVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHCPAPELGGP 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
198 LYSLSVTVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHCPAPELGGP 257
Qy 241 SVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYNS 300
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
258 SVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYNS 317
Qy 301 TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
318 TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 377
Qy 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 420
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
378 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 437
Qy 421 QGNVFCVSNVHEALHNHYTQKSLSLSPGK 449
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
438 QGNVFCVSNVHEALHNHYTQKSLSLSPGK 466

RESULT 11
Q6P055 ID Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
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RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH5820.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ
SEQUENCE 473 AA; 51344 MW; 9816D56A7129B57 CRC64;
      69.2%; Score 2124.5; DB 2; Length 473;
Query Match
Best Local Similarity 88.5%; Pred. No. 7,8e-128;
Matches 402; Conservative 14; Mismatches 33; Indels 5; Gaps 2;
      1 EYTLVESGGDFVKPGSLKVCASGAFSHYAMGVRQTPAKRLEWVAYISS--GGSGT 58
      20 EAHLVESGGGLVRPGSLTLSTGSGFTSGAWLSWVRQAPGKLEWVARIQTEDDGGTT 79
      59 YYSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTY----YFDSNGGGTTL 115
      80 HYGIAGKGRFTVSRDSDRNTLYLQMSLDLTEDTAFYFCATGSMNTVGLTGPDSWGGTTLV 139
      116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
      140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 199
      176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTCPCPAPE 235
      200 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTCPCPAPE 259
      236 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
      260 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 319
      296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYVTLPP 355
      320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYVTLPP 379
      356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 415
      380 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 439
      416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
      440 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 12
Q725W1
ID Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
      69.2%; Score 2124; DB 2; Length 470;
Query Match
Best Local Similarity 89.0%; Pred. No. 8,3e-128;
Matches 404; Conservative 15; Mismatches 27; Indels 8; Gaps 3;
      1 EYTLVESGGDFVKPGSLKVCASGAFSHYAMGVRQTPAKRLEWVAYISSGGSGTY 60
      20 EVQLVESGGGLVQPGSLRLSCVSGFTLNYYDMHVRQGIKGLWVSKIGTAGD-RYY 78
      61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR-----VKLGYVYFDSWGGTTL 115
      79 AGSVKGRFTISRDNKNTLYLQMSLRVGDAAVYICARGAGRWAPLGA--FDIWGQGTNV 136
      116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
      137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
      176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTCPCPAPE 235
      197 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTCPCPAPE 256
      236 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
      257 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 316
      296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYVTLPP 355
      317 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYVTLPP 376
      356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 415
      377 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 436
      416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
      437 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 13
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Q7Z351 PRELIMINARY; PRT; 482 AA.

AC Q7Z351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
GN Name=DKFZp686N02209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]

SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX338118; CAD98026.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
KM
SQ SEQUENCE 482 AA; 52852 MW; ED475F1901D1A034 CRC64;

Query Match 68.7%; Score 2111; DB 2; Length 482;
Best Local Similarity 86.4%; Pred. No. 5.8e-127;
Matches 400; Conservative 19; Mismatches 130; Indels 14; Gaps 2;

Qy 1 EVTLVESGGDFVKPGGSLKVCASAGFAFSHYAMSWVRQTPAKLEWVAYISSGSGTYT 60
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
20 QAQVESGGSVQVQGRSLRLSCLTASGSFGSAMHLRQIPKGLEWAVVISYDGNHKLY 79
Qy 61 SDSVKRGFTTSRDNAKNTLVLMQLSRSEDSAMYFCFR-----VKLGTYT--F 106
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
80 SDSVKRGFTTSRDNSKSLFLHVNLSLTADTAIYCARDFHSHKTSTIFGLIPLFIYSAM 139
Qy 107 DSWGQGTTLVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPPEPTVSNWGALT 166
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
140 DTWGRGTTIVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPPEPTVSNWGALT 199
Qy 167 SGVHTPPAVLQSSGLYLSSLVVTVPSSSLGTHQTVICNVNHKPSNTKVDKKVEPKSCDKTH 226
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
200 SGVHTPPAVLQSSGLYLSSLVVTVPSSSLGTHQTVICNVNHKPSNTKVDKKVEPKSCDKTH 259
Qy 227 TCPPCPAPELLGGPSVFLFPPPKDITLMISTRTEPVTCVVDVSDHEDPEVKFNWYVDGVEV 286
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
260 TCPPCPAPELLGGPSVFLFPPPKDITLMISTRTEPVTCVVDVSDHEDPEVKFNWYVDGVEV 319
Qy 287 HNARKTKPREEQYNSTYRVSVVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 346
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
320 HNARKTKPREEQYNSTYRVSVVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 379
Qy 347 EPQVYTLPISRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPVLDSGSGF 406
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
380 EPQVYTLPISRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPVLDSGSGF 439
Qy 407 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTOKSLSPGK 449
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
440 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTOKSLSPGK 482

RESULT 14

Q6N097 PRELIMINARY; PRT; 481 AA.

ID Q6N097
AC AC Q6N097;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein DKFZp686H20196.	
GN	Name=DKFZp686H20196;	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxId=9606;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RC	TISSUE=Human esophagus tumor;	
RG	The German Human cDNA Consortium;	
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,	
RA	Fobo G., Han M., Wleemann S.;	
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.	
EMBL	EMBL; BX640619; CAB45773.1; -;	
DR	HSSP; P01861; IADQ.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig-cl.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF07654; C1-set; 3.	
DR	SMART; SM00409; Ig; 2.	
DR	SMART; SM00407; IGC1; 3.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG_LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.	
KW	Hypothetical protein_IG_MHC;	
SQ	SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;	

Query Match	67.7%	Score 2080.5;	DB 2;	Length 481;
Best Local Similarity	85.3%	Pred. No. 5.2e-125;		
Matches 394;	Conservative 18;	Mismatches 37;	Indels 13;	Gaps 2

Qy	1	EVTLVESGGDFVPGGSLKVCASGAFAPSHYAMSWROTPAKLEWVAYISSGSGTYY	60
Db	20	QVRLVESGGNVQSGMSRLSCTGSGFSFETYAMHWYRQASGKGLEWLATISFDGGSKIY	79
Qy	61	SDSVKGRFTISRDNAKNTLVLQWRLSESDSAMVFCFTRVK-----LGTY-----FD	107
Db	80	ARSVKGRFVVSRRDNTNSTLFLQWNSLRNTDNTATYYCAKENSAGLLDILSGYFRGWKTVFA	139
Qy	108	SWGQGTTLTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTS	167
Db	140	FWGGTDVSVYASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTS	199
Qy	168	GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHT	227
Db	200	GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHT	259
Qy	228	CPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH	287
Db	260	CPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH	319
Qy	288	NAKTKPREEQNSTYRVSVSLTVLHQDLNKGKEYCKKVSNAKALPAIEKTIISKAKGPQRE	347
Db	320	NAKTKPREEQNSTYRVSVSLTVLHQDLNKGKEYCKKVSNAKALPAIEKTIISKAKGPQRE	379
Qy	348	PQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPVLSDSGFF	407
Db	380	PQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPVLSDSGFF	439
Qy	408	LYSKLTVDKSRWQGNVFSQVMHEALHNHYTKSLSLSPGK	449
Db	440	LYSKLTVDKSRWQGNVFSQVMHEALHNHYTKSLSLSPGK	481

RESULT 15	
Q727P5	
ID	PRELIMINARY; PRT; 469 AA.
AC	Q727P5;
DT	01-OCT-2003 (TrEMBLrel. 25, Created)

RESULT 14	
Q6N097	
ID	Q6N0
AC	Q6N0
DT	05-J

